

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 10:03:29 ; Search time 4879 Seconds
(without alignments)
10447.101 Million cell updates/sec

Title: US-10-626-445-5
Perfect score: 1176
Sequence: 1 atgtcggagtctaacagttac.....accagtcagtatcttcttga 1176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_ov.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_mu.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hgt_hum.*

31: em_hgt_inv.*

32: em_hgt_other.*

33: em_hgt_mus.*

34: em_hgt_pln.*

35: em_hgt_rod.*

36: em_hgt_nam.*

37: em_hgt_vrt.*

38: em_sv.*

39: em_higo_hum.*

40: em_higo_mus.*

41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1176	100.0	1538	10	AF358859	Mus muscu
2	958.4	81.5	1593	10	AF358860	Rattus no
c	821.4	69.8	200346	2	AC131672	Mus muscu
4	686.6	58.4	1173	6	AR142850	Sequence
5	686.6	58.4	1173	6	AR391860	Sequence
6	686.6	58.4	1173	6	AX109119	Sequence
7	686.6	58.4	1173	6	AX139113	Sequence
8	686.6	58.4	1173	6	BD015847	Novel pol
9	686.6	58.4	1173	9	AF325356	Homo sapi
10	686.6	58.4	1173	9	AF329449	Homo sapi
11	686.6	58.4	1173	9	AY008280	Homo sapi
12	686.6	58.4	1173	9	AY136745	Homo sapi
13	686.6	58.4	1173	9	HS2298292	Homo sapi
14	686.6	58.4	1266	6	AX376577	Sequence
15	686.6	58.4	1300	6	AX301229	Sequence
16	686.6	58.4	1312	6	BD095598	Novel gua
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18	686.6	58.4	3689	6	AX549343	Sequence
19	686.6	58.4	3689	9	AF312230	Homo sapi
20	685	58.2	1227	6	BD097512	Novel gua
21	685	58.2	1265	9	AB044934	Homo sapi
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26	613	52.1	1451	10	AF358858	Cavia por
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28	442	37.6	166206	2	AC009668	Homo sapi
c	442	37.6	167296	2	AP002507	Homo sapi
30	442	37.6	169144	9	AC090244	Homo sapi
c	442	37.6	184938	2	AP002476	Homo sapi
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33	271.6	23.1	1326	6	AX451922	Sequence
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35	172.8	14.7	1239	6	E39806	Novel guano
36	172.8	14.7	1242	10	AY009371	Rattus no
37	172.8	14.7	2700	6	E39809	Novel guano
38	150.8	12.8	1339	10	AF267537	Cavia por
39	145.4	12.4	18105	6	BD189979	Use of hi
40	143.8	12.2	2067	10	AY142145	Mus muscu
41	143.8	12.2	2483	10	AY044153	Mus muscu
42	143.2	12.2	1335	10	AF237919	Rattus no
43	143.2	12.2	1338	6	AR104204	Sequence
44	143.2	12.2	1338	6	BD086288	G protein
45	143.2	12.2	1338	10	AY009370	Rattus no

ALIGNMENTS

RESULT 1
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LOCUS AF358859 1538 bp mRNA linear ROD 02-SEP-2001
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358859
VERSION AF358859.1 GI:15420534
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation


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Best Local Similarity 88.4%; Pred. No. 1.5e-260;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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DB 96 TTAATGCTCTCATTTGGCTTTGCTATATAGTGAAGTGTCTGCTGATCTTAGCCTTT 155
QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180
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QY 901 AGGAAGCTAGCAGAGTCTACTGCGCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
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RESULT 3
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LOCUS AC131672
DEFINITION Mus musculus chromosome UNK clone RP23-314021, WORKING DRAFT
ACCESSION AC131672
VERSION AC131672.2 GI:38194370
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 200346)
AUTHORS Wilson,R.K.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 200346)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 200346)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On Nov 6, 2003 this sequence version replaced gi:22475584.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0314021
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing method: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199211 bases at least Q40
Consensus quality: 199561 bases at least Q30
Consensus quality: 199715 bases at least Q20
Insert size: 199000; agarose-fp
Quality coverage: 13.37 in Q20 bases; agarose-fp
Quality coverage: 11.03 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 56: contig of 56 bp in length
* 57 156: gap of unknown length
* 1270: contig of 1114 bp in length
* 1370: gap of unknown length
* 1371 85906: contig of 84536 bp in length
* 85907 86006: gap of unknown length
* 86007 200346: contig of 114340 bp in length.

FEATURES

source

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157..1270
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1371..85906
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ORIGIN

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RESULT 4

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LOCUS AR142850 1173 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6204017.
ACCESSION AR142850
VERSION AR142850.1 GI:15104136
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITLE Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
FEATURES Location/Qualifiers
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ORIGIN

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RESULT 5
AR391860
LOCUS 1173 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6613533.
ACCESSION AR391860
VERSION AR391860.1 GI:40115598
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monisma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
FEATURES Location/Qualifiers
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Source 1. .1173
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ORIGIN

Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGTCCCTTGGCATTT 60
Db 1 ATGCCAGATACTAAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
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Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTGG 420
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RESULT 6
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DEFINITION Sequence 1 from Patent WO0125432.
ACCESSION AXI09119
VERSION AXI09119.1 GI:13924093
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
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ORIGIN
Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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RESULT 7
AXI39113 1173 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION AXI39113
VERSION AXI39113.1 GI:14274791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Peter,B. and O'Reilly,M.A.
TITLE G-protein coupled receptor-like polypeptide
JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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Location/Qualifiers
source
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/mol_type="unassigned DNA"
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/db_xref="taxon:9606"

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Query Match      58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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RESULT 8
BD015847
LOCUS Novel polypeptide. 1173 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:22556984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter, B. and Olaylee, M.A.
TITLES Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PFIZER INC
COMMENT OS Homo sapiens (human)
PN JP 2001211889-A/1
ED 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI
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PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
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RESULT 9
AF325356
LOCUS

DEFINITION	Homo sapiens histamine receptor H4 (AXOR35) mRNA, complete cds.				
ACCESSION	AF325356				
VERSION	AF325356.1 GI:15553202				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1173) Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dycko, G.M., Mannan, I.J., Boyce, R., Alston, J., Tierney, L.A., Li, X., Herrity, N.C., Vawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M., Hieble, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R.				
TITLE	Cloning, expression, and pharmacological characterization of a novel human histamine receptor				
JOURNAL	Mol. Pharmacol. 59 (3), 434-441 (2001)				
MEDLINE	21106320				
PUBMED	11179436				
REFERENCE	2 (bases 1 to 1173) Zhu, Y., Michalovich, D. and Fitzgerald, L.R.				
AUTHORS	Direct Submission				
TITLE	Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box 1539, King of Prussia, PA 19406, USA				
JOURNAL	Location/Qualifiers				
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ACCESSION AF329449
VERSION AF329449.1 GI:13876643

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1173)

Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,

Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,

Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.
and Monsma, F.J. Jr.
Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)

PUBMED

21104636

REFERENCE

2 (bases 1 to 1173)

AUTHORS

Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and

Bayne, M.

TITLE

Direct Submission

Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough

Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,

USA

FEATURES

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Best Local Similarity 75.1%; Pred. No. 2e-183;

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VERSION	AY008280.1 GI:15822540		
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SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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AUTHORS	Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and O'Dowd, B.F.		
TITLE	Discovery of H4, a Novel Histamine Receptor		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1173)		
AUTHORS	Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and O'Dowd, B.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8 Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada		
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LOCUS      Homo sapiens histamine receptor H4 (HRH4) mRNA, complete cds.
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ACCESSION      AY136745
VERSION      AY136745.1 GI:22658472
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ORGANISM      Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (26-JUL-2002) cDNA Resource Center, Guthrie Research
Institute, One Guthrie Square, Sayre, PA 18840, USA
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Query Match      58.4%; Score 686.6; DB 9; Length 1173;
Best local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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ACCESSION AX376577
VERSION AX376577.1 GI:19170678
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1.
Lin,D.C., Zhao,J., Chen,J.L. and Cutler,G.
Novel receptors
TITLE Patent: WO 0200719-A 5 03-JAN-2002;
JOURNAL Tularik Inc. (US)
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Lind,P., Sejlitz,T., Vogeli,G. and Wood,L.S.
G protein-coupled receptors
AUTHORS TITLE Patent: WO 0185793-A 1 15-NOV-2001;
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Job time : 4891 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 10:03:29 ; Search time 557 Seconds
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Title: US-10-626-445-5

Perfect score: 1176

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Listing first 45 summaries

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16	685.2	58.3	1170	8	AAD55126 Human H4
17	685	58.2	1227	6	AAI66009 Human GPR
18	685	58.2	1265	6	AAI66078 Human DNA
19	685	58.2	1265	8	AAD55125 Human H4
20	683.4	58.1	1173	6	AAI67750 Human his
21	613	52.1	1170	6	AAI70983 Guinea pi
22	505.8	43.0	1166	8	AAD55124 Human H4
23	436.6	37.1	1103	8	AAD55123 Human H4

ALIGNMENTS

RESULT 1

AAI70981
ID AAI70981 standard; cdna; 1176 BP.

XX
AC AAI70981;

XX
DT 18-MAR-2002 (first entry)

XX
DE Mouse histamine H4 receptor cdna.

XX
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.

XX
OS Mus musculus.

XX
PV W0200192485-A1.

XX
PD 06-DEC-2001.

XX
PF 22-FEB-2001; 2001WO-US005914.

XX
PR 31-MAY-2000; 2000US-0208260P.

XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX
PI Lovenberg T, Liu C;

XX
DR WPI; 2002-114339/15.

XX
DR P-PSDB; AAM50565.

XX
New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

XX
PS Claim 4; Fig 5A; 92pp; English.

XX
The present sequence is that of a cdna clone encoding a murine histamine receptor of the H4 subtype. The cdna was isolated from a mouse spleen cDNA library. It shows 72.8% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of

Aad37667 Human G-p
Aas98150 Human DNA
Aax84570 G-protein
Aaa70639 Rat G-pro
Aax84571 G-protein
Aaa70640 Rat G-pro
Aal59979 Human H3
Aal59985 Human H3
Abz82337 Mouse his
Aah44575 Rat musca
Aaa70638 Rat G-pro
Abt42301 Toxicity
Aax59168 Rat G pro
Aah44574 Rat musca
Abx11853 Rat cdna
Aah47749 Human his
Aal59977 Human H3
Aal59976 Human wil
Aah26798 Human his
Aah44573 Human mus
Aax02886 Human mAC
Aaa09062 Human his

24 271.6 23.1 1326 6 AAD37667
25 269 22.9 540 6 AAS98150
26 172.8 14.7 1239 3 AAX84570
27 172.8 14.7 1239 3 AAA70639
28 172.8 14.7 2700 2 AAX84571
29 172.8 14.7 2700 3 AAA70640
30 171.6 14.6 1311 8 AAL59979
31 168.6 14.3 1203 8 AAL59985
32 145.4 12.4 18105 7 ABZ82337
33 143.2 12.2 1338 2 AAH44575
34 143.2 12.2 1953 3 AAA70638
35 143.2 12.2 2761 7 ABT42301
36 143.2 12.2 3244 2 AAX59168
37 143.2 12.2 3244 2 AAH44574
38 143.2 12.2 3244 7 ABX11853
39 142 12.1 1098 4 AAH47749
40 142 12.1 1161 8 AAL59977
41 142 12.1 1401 8 AAL59976
42 140.4 11.9 1023 4 AAH26798
43 140.4 11.9 1334 2 AAH44573
44 140.4 11.9 1335 2 AAX02886
45 140.4 11.9 1335 3 AAA09062

CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptor activity. Recombinant protein is useful for identifying
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be
 CC useful for diagnosing, treating or preventing asthma, allergy,
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
 CC disorders of the neuroendocrine system, stress and spasticity
 XX
 SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

Query Match 100.0%; Score 1176; DB 6; Length 1176;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGGAGCTTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60
 DB 1 ATGTCGGAGCTTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60

QY 61 TTAATGCTCTTCAATTTGGCCCTTTGCTATATAATGTTAGGCAATGCTGTGCTCATCTTAGCCCTTT 120
 DB 61 TTAATGCTCTTCAATTTGGCCCTTTGCTATATAATGTTAGGCAATGCTGTGCTCATCTTAGCCCTTT 120

QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180
 DB 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180

QY 181 GACTTCCCTCGTGGTGTGATTTCCATTTCTCTGTACATCCCTCAGTGTGTTAACTGG 240
 DB 181 GACTTCCCTCGTGGTGTGATTTCCATTTCTCTGTACATCCCTCAGTGTGTTAACTGG 240

QY 241 AATTTTGGAAAGTGGAAATCGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
 DB 241 AATTTTGGAAAGTGGAAATCGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300

QY 301 TCTGCTCAATATTTGCTCCTAATAGCTACGATCGAATACCACTGCTGTTTCAATGCTGTG 360
 DB 301 TCTGCTCAATATTTGCTCCTAATAGCTACGATCGAATACCACTGCTGTTTCAATGCTGTG 360

QY 361 TCTTATAGGCTCAACACACTGGCATCATGAGATTTGTTGCTCAATGCTGCTGTTGG 420
 DB 361 TCTTATAGGCTCAACACACTGGCATCATGAGATTTGTTGCTCAATGCTGCTGTTGG 420

QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTGGCTTCAATGCTGCTGTTGG 480
 DB 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTGGCTTCAATGCTGCTGTTGG 480

QY 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGTGTACATCTCCACATTACA 540
 DB 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGTGTACATCTCCACATTACA 540

QY 541 ATGCTCTTGGAAATTCCTGCTTCTCTGCTATCTCTGCTGCTTATTTCAATGCTACAGATTAC 600
 DB 541 ATGCTCTTGGAAATTCCTGCTTCTCTGCTATCTCTGCTGCTTATTTCAATGCTACAGATTAC 600

QY 601 TGGAGCTGTGGAAGCTAGGCTCTCTCAGTAGGTGCCCTTAGCCATGCTGATTTCCACT 660
 DB 601 TGGAGCTGTGGAAGCTAGGCTCTCTCAGTAGGTGCCCTTAGCCATGCTGATTTCCACT 660

QY 661 ACCTCTTCAGTGTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
 DB 661 ACCTCTTCAGTGTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720

QY 721 CCTGATTTGAAGAAATCAGCTGCATCTCTGCTACTGAGAAAGTCTCTGAGAAAGAGCAGC 780
 DB 721 CCTGATTTGAAGAAATCAGCTGCATCTCTGCTACTGAGAAAGTCTCTGAGAAAGAGCAGC 780

QY 781 ATCTGGTGTCTTAAAGACTCACATGAACAGCAGTATCACTGCTTCAAGTGGTTCC 840
 DB 781 ATCTGGTGTCTTAAAGACTCACATGAACAGCAGTATCACTGCTTCAAGTGGTTCC 840

QY 841 TTCTGGCGATCGGAAGTGCAGGCTTCCGCCAAGGGAGTACGACAGCTTCTCAGAGC 900
 DB 841 TTCTGGCGATCGGAAGTGCAGGCTTCCGCCAAGGGAGTACGACAGCTTCTCAGAGC 900

QY 901 AGGAGCTAGCCAGCTCACTGGCCATCCTTCTGAGGCTTTTGGCCATTTGCTGGGCTCCA 960
 DB 901 AGGAGCTAGCCAGCTCACTGGCCATCCTTCTGAGGCTTTTGGCCATTTGCTGGGCTCCA 960

QY 961 TACTGTCTGTTTCACTAATTTGCTCTTCACTTACCCACAGAACGAGAACGAGTGTG 1020
 DB 961 TACTGTCTGTTTCACTAATTTGCTCTTCACTTACCCACAGAACGAGAACGAGTGTG 1020

QY 1021 TGGTACAGATTGGCTTCTGCTGCAATGGTTCAATTCGTTTAAATCCCTTCTGTAC 1080
 DB 1021 TGGTACAGATTGGCTTCTGCTGCAATGGTTCAATTCGTTTAAATCCCTTCTGTAC 1080

QY 1081 CTTTGTGTGTCACAGGCTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
 DB 1081 CTTTGTGTGTCACAGGCTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140

QY 1141 CCAGCGCTGTCTACAGAACCCAGTCAGTATCTTCTTGA 1176
 DB 1141 CCAGCGCTGTCTACAGAACCCAGTCAGTATCTTCTTGA 1176

RESULT 2
 AAI70982
 ID AAI70982 standard; cdna; 1176 BP.
 AC AAI70982;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE Rat histamine H4 receptor cdna.
 XX
 KW Histamine H4 receptor; rat; antisthmatic; antiallergenic;
 KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
 KW diagnosis; gene therapy; ss.
 XX
 OS Rattus rattus.
 XX
 PN WO200192485-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 22-FEB-2001; 2001WO-US005914.
 XX
 PR 31-MAY-2000; 2000US-0208260P.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 PI Lovenberg T, Liu C;
 XX
 WPI: 2002-114339/15.
 DR P-PSDB; AAM50566.
 DR
 XX
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.
 XX
 PS Claim 4; Fig 5C; 92pp; English.
 XX
 CC The present sequence is that of a cdna clone encoding a rat histamine
 CC receptor of the H4 subtype. The cdna was isolated from a rat spleen cdna
 CC library. It shows 72.5% homology to the human H4 receptor coding region.
 CC The invention provides mammalian (human, mouse, rat and guinea pig)
 CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
 CC recombinant host cells that produce active recombinant protein. The
 CC pharmacology of known histamine ligands is demonstrated. Mammalian
 CC histamine H4 receptor may be used in gene therapy for the treatment of
 CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptor activity. Recombinant protein is useful for identifying
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be
 CC useful for diagnosing, treating or preventing asthma, allergy,
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin

CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
CC disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;
Query Match 81.5%; Score 958.4; DB 6; Length 1176;
Best Local Similarity 88.4%; Pred. No. 1.2e-289;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCCACCAGCTGCTCAGGTCCTTGGCAATTT 60
Db |||||
QY 1 ATGTCGGAGTCTAACGGCACTGAGCTCTTGCCACTGCTCAGTCAAGTCCCTTGGCAATTT 60
Db |||||
QY 61 TTAATGTCCTTCATTGCTCTTGTATATATGATGGTGAATGCTGGTCACTTAGCCCTTT 120
Db |||||
QY 61 TTAATGTCCTCTGCTTGTCTTTGTATTAACATAGCAATGCTGGTCACTTAGCCCTTT 120
Db |||||
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT 180
Db |||||
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT 180
Db |||||
QY 181 GACTTCCTGCTGGGTTGATTTTCATTCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
Db |||||
QY 181 GACTTCCTGCTGGGTTGATTCCTCATTCCCTGTACATCCCTCAGCTGTTTAACTGG 240
Db |||||
QY 241 AATTTTGGAGTGAATCTGCATGTTTGGTCACTACTACTGACTATCTTTTGTGCCCGCA 300
Db |||||
QY 241 AATTTTGGAGTGAATCTGCATGTTTGGTCACTACTACTGACTATCTTTTGTGCCAGCA 300
Db |||||
QY 301 TCTGTCTACAAATATTTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAAATCTGTG 360
Db |||||
QY 301 TCCGCTACAGTATTTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAAAGCTGTG 360
Db |||||
QY 361 TCTTATAGGCTCAAACACTGGCATCATGAAGATTTGCTCAATGTTGGTGGCTGTTGG 420
Db |||||
QY 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGCTCAATGTTGGTGGCTGTTGG 420
Db |||||
QY 421 ATACTGGCTTCTTGGTAATGCCCCGATCTGCTGCTTCAATCTTCTGTAAGAACAGC 480
Db |||||
QY 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATCTTGGAAAGAACAGC 480
Db |||||
QY 481 ACAGAACAAAGGACTGTGAGCTGGCTTGTGTACAGAGTGGTACATCTCCACCATTAACA 540
Db |||||
QY 481 ACCAACACAGAGAGTGGAGCTGGCTTGTGTACTGAGTGGTACATCTCCGCAATTAACA 540
Db |||||
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTGTCATCTCTGTGGCTTATTTCAAGTACAGATTTAC 600
Db |||||
QY 541 GCATTTCTTGGAAATTCCTGCTTCTGTGTCATCTCTGTGGCTTATTTCAAGTACAGATTTAC 600
Db |||||
QY 601 TGGAGCTGTGGAGCTGAGGCTCTCAGTAGGTGCTCAGTACGCTAGCCATGCTGATTTCTCCACT 660
Db |||||
QY 601 TGGAGCTGTGGAGCTGAGGCTCTCAGTAGGTGCTCAGTACGCTAGCCATGCTGATTTCTCCACT 660
Db |||||
QY 661 ACCTCTTCCAGTGTCTCAGGACACTACAGAGCTGGGCTGGCTTGCAGGACAAAGTAAT 720
Db |||||
QY 661 ACCTCTTCCAGGACACTGAGACACTACGAGAACTGGTGGCTTGTAGGACAAAGTCTT 720
Db |||||
QY 721 CCTGGATTAAGGAATCAGCTGATCTGCTGTCATCTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Db |||||
QY 721 CCTGGATTAAGGAATCAGCTGATCTGCTGTCATCTCAGAAAGTCTCGAAGAAAGAGCAGT 780
Db |||||
QY 781 ATCTGTGTCTTAAAGGACTCAATCAACAGCAGTATCACTGCTTCAAGTGGGTTCC 840
Db |||||
QY 781 CTCTGTGTCTTAAAGGACTCAATCAGCGGTAGTATCATCGCTTCAAGTGGGTTCC 840
Db |||||
QY 841 TTCTGGCGATCGAAAGTGGAGCGCTTCGGCAAGGAGTACGAGAGCTTCTCAGAGGC 900
Db |||||
QY 841 TTCTGGCGATCAGAAAGCCAGTCTTCCAGCAGAGAGCAGCTGAGCTTCTCAGAGGC 900
Db |||||
QY 901 AGAAGCTAGCAGGCTCAGTGGCCATCTCTGTAGCGCTTTTGGCAATTTGCTGGGCTCCA 960
Db |||||
QY 901 AGGAAGCTAGCAGGCTCAGTGTCTCTCTGAGTGTCTTGTGCAATTTGCTGGGCTCCG 960
Db |||||

QY 961 TACTGTCTGTTCACAAATGTCTTCAACTTACCAGAAAGCGCCCAAAATCGGTG 1020
Db |||||
QY 961 TATGCTGTTCACAAATGTCTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGAAT 1020
Db |||||
QY 1021 TGGTACAGCAATTCCTTCTGCTGCAATGTTCAATTCGTTTGTATATCCCTTTCTGTAC 1080
Db |||||
QY 1021 TGGTACAGCAATAGCTTTTGGCTACAGTGTCTCAATTCACCTTATTAATCCCTTTCTATAC 1080
Db |||||
QY 1081 CCTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
Db |||||
QY 1081 CCTTGTGTCCACAGAGCTTTCCAGAAAGGCTTTCTGGAAGATCTCTGTGTGACAAAGCAA 1140
Db |||||
QY 1141 CCAGCGCTGTCAAGAACACAGTCAGTATCTCTTGA 1176
Db |||||
QY 1141 CCAGCACCTTCAGAGACCCAGTCAGTATCTTCTTGA 1176
Db |||||
RESULT 3
AAA46023
ID AAA46023 standard; cDNA; 1173 BP.
XX
AC AAA46023;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hrup7 encoding cDNA SEQ ID NO:13.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-US024065.
XX
PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 28-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX
PA (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI; 2000-317986/27.
DR P-PSDB; AAB02831.
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX Example 1; Page 88-89; 187pp; English.
XX The present invention describes transmembrane receptors, preferably human
CC protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
QY 1 ATGTCGGAGCTTAACAGTACTGGGATCTTGGCCACAGCTGCTCAGGTCGCCCTTGGCAATTT 60
DB 1 ATGTCAGAGATCAATAGCAGCAATCAATTTATCACTAAGCACTCGGTGTACTTTAGCAATTT 60
QY 61 TTAATGCTCTTCAATTTGGCTTCTATATGAGTGGCAATGCTGTGATCTTAGCCCTTT 120
DB 61 TTAATGCTCTTAGTACTTTTCTATATGAGTGGCAATGCTGTGATCTTAGCTTTT 120
QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAAATTTGGCTATTTCT 180
DB 121 GTGTGGACAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACTTGGCCATCTCT 180
QY 181 GACTTCTCTGGTGGTGGTATTTCCATCTCTGTACATCCCTCAGTGTGTTAACTGG 240
DB 181 GACTTCTTTGTGGTGGTGGTATCTCCATCTCTGTATCCCTCAGTGTGTTAACTGG 240
QY 241 AATTTTGGAGTGGATCTGCAATGTTTGGCTCAATTAATCTTCTTAACTTGGCCAGCA 300
DB 241 GAATTTGGAGAAATCTGTATTTTGGCTCAATTAATCTTCTTAACTTGGCCAGCA 300
QY 301 TCTGTCTACAATTTGCTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
DB 301 TCTGTATATAACATTTGCTCTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
QY 361 TCTTATAGGCTCAACACTGGCATCATGAAGATTTGCTCAATTAATTAATTAATTAAT 420
DB 361 TCTTATAGAACTCAACACTGGGCTCTTGAAGATTTGCTCAATTAATTAATTAATTAAT 420
QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAATTAATTAATTAATTAAT 480
DB 421 GTGCTGGCTTCTTGTAGTAAATGGCCGATGATTTCTAGTTCAGAGCTTTGGAGGA --- 476
QY 481 AGAACAACAAAGGACTGTGAGGCTGGCTTTGTTTACAGAGTGATCATCTCTACCAATTACA 540
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGCCATACA 534
QY 541 ATGCTCTTGGATTTCTGCT 600
DB 535 TCATTTCTTGGAAATCGTGAATCCAGTCACTTTAGTGTCTTATTTCAACATGAATATTTAT 594
QY 601 TGGACCTCTTGAAGCTGTAGGCTCTCAGTAGTGCCCTTAGCCATGCTGGATTTCTCCACT 660
DB 595 TGGACCTCTTGAAGGCTGATCATCTCAGTAGTGCCCAAGCCATCTCTGACTGCTGCT 654
QY 661 ACCTCTTCCAGTCTTCAGGACACTTACAGAGCTGGGGTGGCTTGCAGGCAAGTAAT 720

DB 655 GTCTCTTCCACATCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CTGTGATTTGAAGGAATCAGCTGACTCTCTGCTACTCAGAAAGTCTCTGAGAAAGACGAC 780
DB 715 TCTGCATCAGACAGAAAGTTCTCTGATCTCTCTGATCTCTCTTCAATTCAGAGAGACAGAGGAGAAAGAGTAGT 774
QY 781 ATCTGGTGTCTTAAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAAGTGGTTC 840
DB 775 CTATGTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834
QY 841 TTTGGCCATCGAAAGTGCAGCGCTTCGCAAGGGAGTAGCGCAGAGCTTCTCAGAGGC 900
DB 835 TTTCTCCCAATCAGATTTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTGCTTAGAGGC 894
QY 901 AGGAGCTAGCCAGCTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGTCCA 960
DB 895 AGGAGTAGCCAGCTCAGTGGCCATCTTCTGAGCGCTTTTGGCTTTTGGTGGGTCCA 954
QY 961 TACTGTCTGTTCACAAATTTGCTCTTCAACTTACCCAGAGCGGACGCGCCCAAAATCGGTG 1020
DB 955 TATCTCTGTTCACAAATTTGCTCTTCAATTTATCTCTCAGCAACAGGTCCTAAATCAGTT 1014
QY 1021 TGGTACAGATTTGCTCTGCTGCAATGCTTCAATTTGCTTGTAACTCTTCTCTGTAC 1080
DB 1015 TGGTATGAATTTGCAATTTTGGCTTCAAGTGTCAATTTCTTGTCAATCTCTTTTGTAT 1074
QY 1081 CTTTGTCTCAGAGCGCTTCCAGAGCGCTTCTGGAAGACTTCTGGAAGACTTCTGTCAGCAAGCAA 1140
DB 1075 CCAATTTGTCAAGCGCTTTCAAAGCGCTTTCTTGAAGAAATTTTGTATATAAAGCAA 1134
QY 1141 CCAGCGCTGTCCACAGAAC --- CAGTCAGTATCTCTTGA 1176
DB 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173
RESULT 4
AAB01124
ID AAB01124 standard; cDNA; 1173 BP.
XX AC AAB01124;
XX DT 02-NOV-2000 (first entry)
XX Human orphan G protein-coupled receptor hrUP7 cDNA.
XX DE Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;
KW transmembrane receptor; signal cascade; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 1..1173
XX FT /*tag= a
FT /product= "hrUP7"
FT /note= "Human orphan G protein-coupled receptor"
XX PN WO200031258-A2.
XX PD 02-JUN-2000.
XX PF 13-OCT-1999; 99WO-US023687.
XX PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 29-SEP-1999; 99US-0156555P.
 PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156653P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157293P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 XX Chen R, Dang HT, Liaw CW, Lin I;
 XX
 DR WPI; 2000-400068/34.
 DR P-PSDB; AAY71297.
 XX
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for
 PT use in the identification of G protein-coupled receptor agonists.
 XX
 PS Claim 25; Page 59; 102pp; English.
 XX
 CC The present sequence is a cDNA encoding hrup7, an endogenous human orphan
 CC G protein-coupled receptor (GPCR). The full length hrup7 cDNA was cloned
 CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
 CC GPCR of the invention, like all GPCRs has seven transmembrane alpha
 CC helices with an extracellular N-terminus and an intracellular C-terminus.
 CC However, no endogenous ligands has yet been identified for the proteins
 CC of the invention. The orphan GPCRs may be used in the identification of
 CC their endogenous ligands, and to screen potential GPCR agonists and
 CC antagonists for use as pharmaceutical agents. The proteins may also be
 CC used in the study of GPCR-mediated signalling cascades, and to elucidate
 CC their precise role in normal and diseased human conditions. Nucleic acid
 CC encoding human orphan GPCRs may be used for tissue localisation
 CC expression analysis to provide information about their function in
 CC healthy and pathological states
 CC
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Query Match 58.4%; Score 686.6; DB 3; Length 1173;
 Best Local Similarity 75.1%; Pred. No. 2.4e-204;
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
 QY 1 ATGTGGAGTCTAACAGTACTGGCATCTGCCACAGCTGCTCAGGTCCTTGGCATTT 60
 DB 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTAGCATTT 60
 QY 61 TTAATGCTTCATTTGGCTTTGCTATTAATGTTAGGCAATGCTGGTCATCTTAGCCTTT 120
 DB 61 TTTATGCTCTTAGTGTCTTTTGTATTAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120
 QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAAATTTATTTTCTTAATTTGGCTATTCT 180
 DB 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCACTCT 180
 QY 181 GACTTCTCTGGTGTGATCTCAATCTCTGTACATCCCTCACAGCTGTTTGAATCG 240
 DB 181 GACTTCTCTGGTGTGATCTCAATCTCTGTACATCCCTCACAGCTGTTTGAATCG 240
 QY 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCAATCTGACTATCTTTTGTGACCGCA 300
 DB 241 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
 QY 301 TCTGTCTACAAATATGTCCTCATTTAGCTAGCATCGATACAGTCAGTTCAATGCTGTG 360
 DB 301 TCTGTATTAACATTTGCTTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360
 QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTCCTAAATGGTGGCTTTTGG 420

Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCGGTTTGG 420
 QY 421 ATACTGGCTTTCTTGGTAAATGSCCGCATGATTTCTGGCTTCAGATTCTTGGAAAGAACAGC 480
 Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGGAAGGA 476
 QY 481 ACGAAACAAAGGACTGTGTAGCCCTGGCTTTGTGTACAGAGTGGTACATCTCCACCATTACA 540
 Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTTCCATCACA 534
 QY 541 ATGCTCTTGAATTCCTGGCTTCTGTCACTCTGTGGCTTTATTTCAATGTACAGATTTC 600
 Db 535 TCATTCTTGAATTCGTGATCCAGTCATCTTAGTGGCTTTATTTCAACATGAATATTAT 594
 QY 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCGCTAGCCATGCTGATTTCTCCTC 660
 Db 595 TGGAGCGCTGTGGAAGCGTGTATCTCTCAGTAGGTGCGCAAGCCATCTCTGGAGTACTGCT 654
 QY 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTTCAGGACAAAGTAAT 720
 Db 655 GTCTCTTCCAACTGTGTGGACACTATTCTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
 QY 721 CCTGGATTGAAGAAATCAGCTGCTCATCTCGTCACTCAGAAAAGTCTCTCGAAGAAAGAGCAGC 780
 Db 715 TCTGCACTCGACAGAAAGTCTCTGCTCATCTTCAATTCAGAGACAGAGAGGAGAGTAGT 774
 QY 781 ATCTGTGTCTCTTAAAGGACTCATGAAACAGCAGATGATCACTGCTTCAAAGTGGGTTC 840
 Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATAAATGCTTCCAAAATGGGTTC 834
 QY 841 TTCTGGCGATCGGAAGTGTGAGCGCTTTCGCAAGGGAGTACGAGAGCTTCTCAGAGGC 900
 Db 835 TTCTCCCAATCAATCTGTAGCTCTTCAACAAAGGGAACTGTTGACTGCTTAGAGCC 894
 QY 901 AGAAGCTAGCCAGGCTCAGTGGCCATCTTCTCAGGCGCTTTTCCCATTTCTGGGCTCCA 960
 Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTTCTGGGCTCCA 954
 QY 961 TACTGTCTGTTCACAAATGTCTTCACTTCACTCCCAAGAGGAAACGCTTGTGAGTGTG 1020
 Db 955 TATTCTGTCTCAAAATGTCTTCAATTTATTTCTCAGCAACAGGTCCTCAATCAGTT 1014
 QY 1021 TGTGTACAGCATTCCTTCTGGCTGCAATGTTCAATTTCTGTTTGTATCTCTTCTGTAC 1080
 Db 1015 TGTGTATAGATTGCAATTTTGGCTCAGTGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
 QY 1081 CCTTGTGTACAGGCGTTTCCAGAGGGCTTCTGGAAGATACCTTTGTGACAAAGCAA 1140
 Db 1075 CCATTGTGTACAGGCGTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAAGCAA 1134
 QY 1141 CCAGCGCTGTACAGAAC---CAGTCAATGATCTTCTTGA 1176
 Db 1135 CCTCTACCATCACACACAGCTGCTGCTCAGTATCTTCTTAA 1173
 RESULT 5
 AAF83203
 ID AAF83203 standard; cDNA; 1173 BP.
 XX
 AC AAF83203;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DE Human GPCR-like polypeptide, PFI-013 encoding cDNA.
 XX
 KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;
 KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
 KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;
 KW signal transduction; ss.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers

```

CDS
1. .1173
/*tag= a
/product= "PFI-013"
EPI096009-Al.
XX
PD 02-MAY-2001.
XX
PF 24-OCT-2000; 2000EP-00309364.
XX
PR 29-OCT-1999; 99GB-00025641.
XX
PR 20-APR-2000; 2000GB-00009973.
XX
PA (PFIZ ) PRIZER LTD.
XX
PA (PFIZ ) PRIZER INC.
XX
PI Peter B, O'reilly MA;
XX
DR WPI; 2001-309854/33.
XX
DR P-PSDB; AAB62445.
XX
PT New G-protein coupled receptor-like polypeptide, polynucleotide for
PT screening drug candidates for treating diseases associated with signal
PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
PS Claim 1; Page 43; 66pp; English.
XX
CC This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
CC expressed by standard recombinant methodology. Antibodies and modulators
CC of PFI-013 are useful in the manufacture of a medicament for treating
CC allergic disorder, including extrinsic asthma, immunological disorders,
CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial
CC and other pulmonary disease, including chronic obstructive pulmonary
CC disease (COPD), infectious, inflammatory disease, such as inflammatory
CC bowel disease and neoplastic and myeloproliferative diseases. They are
CC also useful for treating obesity, diabetes, metabolic, neurological
CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual
CC medicine, inflammation, cancer, tissue repair, dermatology, photoageing,
CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
CC diseases, allergy and respiratory disease, sensory organ disorders, sleep
CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful
CC in the diagnosis and treatment of the above conditions and also for
CC screening drug candidates for the treatment of diseases associated with
CC signal transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 58.4%; Score 686.6; DB 4; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
QY 1 ATGCGGAGTCTTAACAGTACTGGCATCTTGGCCACGAGTGTCTCAGGTCCCTTGGCATTT 60
DB 1 ATGCGAGATACCTAATAGCACAATCAATTTATCACTAAGCAGCTCGTGTACTTTAGCATTT 60
QY 61 TTAATGCTCTCAATTTGGCTTGGTATATGAGTGAAGTGTGCTGCTATCTTAGCCTTT 120
DB 61 TTAATGCTCTTAGTAGTCTTTGGTATATGAGTGAAGTGTGCTGCTATCTTAGCCTTT 120
QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCT 180
DB 121 GTGGTGGACAAACCTTAGACATCGAAGTATTTTCTTAATTTGGCCATCTCT 180
QY 181 GACTTCTCGTGGGTTGATTTCCATTCCTCTGTACATCCCTCAACGTTGTTTAACTGG 240
DB 181 GACTTCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAACGCTGTTTCAATGG 240
QY 241 AATTTTGGAGTGGATCGCATGTTTGGCTGCTACTGACTATCTTTTGTGCCACGCA 300
DB 241 GATTTTGGAAAGGAAATCTGTGTTATTTTGGCTCACTGACTATCTGTATGTACAGCA 300

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QY 301 TCTGTCTACAATAATGTGTTCTCATTTAGCTACGATCGATACCACTCAGTTTCAAATGCTG 360
DB 301 TCTGTATATAACATTTGTTCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACACTGGGATCATGAAGATGTTGCTCAAAATGGTGGCTGTTGG 420
DB 361 TCTTATAGAACTCAACATCTAGGCTCTTGAAGATTTGTTACTCTGATGGTGGCCGTTGG 420
QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATCTTGGCTTCAGATTTCTTGGGAAGACAGC 480
DB 421 GTGCTGGCTTCTTGTAGTGAATGGGCAATGATTTCTAGTTTCAGATCTTGGAGGA---- 476
QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGTGATCATCTCCATTCACA 540
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCTCTTGGCCATCACA 534
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
DB 535 TCAITTTTGGAAATTCGTCATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
QY 601 TGGAGCCTGTGMAAGCGTAGGCTCTCAGTAGGTCCCTAGCATGCTGGATTTCTCCACT 660
DB 595 TGGAGCCTGTGMAAGCGTAGTCATCTCAGTAGGTCCAAAGCCATCTTGGACTGACTGCT 654
QY 661 ACCTCTTCCAGTGTCTTCAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGTCC 720
DB 655 GTCCTCTTCCACATCTGTGGACACTCAITTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGATTTGAAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 715 TCTGATCGACAGAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
QY 781 ATCTGCTGCTTCAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGTCC 840
DB 775 CTATGTTTCTTCAAGAACCAAGATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 834
QY 841 TTTCTGGCATCGMAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGCAGAGCTTCTTCAGAGGC 900
DB 835 TTTCTCCCAATCAGATTTCTGTAGCTTCTTCCAAAGGGAAACATGTTGAACCTGCTTAGAGCC 894
QY 901 AGGAAGCTAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 895 AGGAGATTTAGCAAGTCACTGCGCATCTCTTCTAGGGGTTTTTGTGCTGTTTGGGCTCCA 954
QY 961 TACTGCTGTTCACAATTTGCTTCTTCAACTTACCCAGAACGGAACGCCCAAAATCGGTG 1020
DB 955 TATCTCTGTTCACAATTTGCTTCTTCAACTTATTTTCTCAGCAGCAGGCTCTTAATCAGTT 1014
QY 1021 TGGTACAGCATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1015 TGGTATAGAAATTTGCAATTTTGGCTTTCAGTGGTTCATTTCTTGTGCTCAATCTCTTTGTAT 1074
QY 1081 CTTTGTGTGACAGCGGTTTCCAGAGGCTTTCAGAGGCTTTCGGAAGATGCTTGTGTGACAAAGCAA 1140
DB 1075 CCAATTTGTGTCACAGCGCTTTCAAAGGCTTTCTTGAAGATATTTTGTATAAAAAAGCAA 1134
QY 1141 CCAGCGCTGTCAACAGAAC---CAGTCAGTATCTCTTGA 1176
DB 1135 CCTCTACCATCAACACAGCTCGGTGCTGATGCTTCTTAA 1173

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RESULT 6

AAH24007

ID AAH24007 standard; cDNA; 1173 BP.

XX AAH24007;

XX 10-AUG-2001 (first entry)

XX Human G protein-coupled receptor AXOR35 cDNA.

XX AXOR35; human; G protein-coupled receptor; 7TM receptor;

histamine H3 receptor homologue; infection; viral; bacterial; fungal; protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delirium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery; ss.

Homo sapiens.

Key Location/Qualifiers
 CDS 1..1173
 /tag= a
 /product= "Human AXOR35"
 /note= "G protein-coupled receptor"

WO200133221-A1.
 10-MAY-2001.
 26-OCT-2000; 2000WO-US029461.
 02-NOV-1999; 99US-00431898.
 03-FEB-2000; 2000US-00497790.
 (SMK) SMITHKLINE BEECHAM CORP.
 (SMK) SMITHKLINE BEECHAM PLC.

Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X; Michalovich D, Morrow DM, Zhu Y; WPI: 2001-316464/33.
 P-PSDB; AAB73622.

Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.

Claim 2; Page 49-50; 54pp; English.

The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to cDNA encoding AXOR35 (AAB74006), and to AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative transmembrane domains and is involved in signal transduction. AXOR35 has homology and structural similarity with G protein-coupled receptors such as the human histamine H3 receptor. The invention also relates to expression vectors and host cells comprising AXOR35 DNA, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR35 activity or expression. Such AXOR35 modulators are particularly useful for treating asthma, and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils or neutrophils in asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via the detection of mutations in the corresponding gene. AXOR35 proteins are

CC also useful for inducing an immunological response in a mammal against
 CC the above diseases, and for antibody production. AXOR35 nucleotides are
 CC also useful as diagnostic reagents, in chromosome localisation and tissue
 CC expression studies, and for producing transgenic animals useful in drug
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
 CC protein or fragments thereof, and are also useful for treating conditions
 CC associated with the expression of the AXOR35 protein. The present
 CC sequence represents cDNA encoding human AXOR35

XX
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Query Match 58.4%; Score 686.6; DB 5; Length 1173;
 Best Local Similarity 75.1%; Pred. No. 2.4e-204;
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACACAGTACTGGGATCTTGGCCACACAGCTGCTCAGGTCCCTTGGCATTTT 60
 DB 1 ATGCCAGATACTAATAGCACAATCAATTTATCATCAAGCACTCGGTGTACTTTAGCATTT 60
 QY 61 TTAATGTCCTTCATTGCGCTTTGCTATATAGTGGAGCAATGCTGTGTCATCTTAGCCTTTT 120
 DB 61 TTTATGTCCTTAGTAGCTTTTCTATATAGCTAGGAATGCTTGTGTCATTTTAGCTTTT 120
 QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
 DB 121 GTGTGGACAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGCCCATCTCT 180
 QY 181 GACTTCCTCGTGGTGTGATTTCCATTCCTCTGTACACACCCCTCAGCTGTGTTAACTGG 240
 DB 181 GACTTCCTTTGTGGTGTGATCTCCATTCCTTTGTATACCTCCCTCACACGCTGTTCGAATGG 240
 QY 241 AATTTTGGAGTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCAACGCA 300
 DB 241 GAATTTGGAAAGAAATCTGTGTAATTTTGGCTCAGTACTGACTATCTGTTATGTACAGCA 300
 QY 301 TCTGTCTACAATATTTGCTCTCATTTAGCTACGATCCGATACAGTCTAGTTTCAATGCTGTG 360
 DB 301 TCTGTATATACATTTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360
 QY 361 TCTTATAGCGCTCAACACACTGGGCAATCATGAAGATGTTTGTCTCAATGCTGTGTTGG 420
 DB 361 TCTTATAGAACTCAACATACTGGGCTCTTGAAGATGTTTACTCTGATGCTGGCGTTTGG 420
 QY 421 ATACTGGCTTTCTTGTAAATGGCCGATGATTTCTGGCTTCAGATTCTTGGAGACAGC 480
 DB 421 GTGCTGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGAGTCTTTGGAAGGA --- 476
 QY 481 ACGAACAACAAAGGAGCTGTGAGCTCGCTTTTGTACAGAGTGTGTACATCCTCAACATTA 540
 DB 477 --TGAAGGTAGTGAATGTGAACCTGGAATTTTTCGGAATGTTACATCCTTCCCATCA 534
 QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTATCTCTGTGGCTTATTTCAATGTACAGATTTCAC 600
 DB 535 TCAATCTTTGGAATTCGTATCCAGTCCAGTCACTCTTAGTGGCTTATTTCAACATGAATAT 594
 QY 601 TCGAGCTGTGCAAGCGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGGATTTCTCCACT 660
 DB 595 TGGAGCTGTGGAAGCGTGATCATCTCAGTAGGTGCAAAAGCCATCCTGGACTGACTGCT 654
 QY 661 ACCTCTTCCAGTCTTCAGGACACTTACACAGCTGGGGTGGCTTTTCAGAGGACAAAGTAAT 720
 DB 655 GTCTCTTCCAACATCTGTGGACACTCATTTACAGAGTAGACTATCTTCAAGGAGATCTCT 714
 QY 721 CTGGAATGAAGGAATCAGTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
 DB 715 TCTGCATCGACAGAAGTTCCTGCATCTCTTTCATTTCAGAGACAGAGAGAGAGAGTAGT 774
 QY 781 ATCTCGTGTCTCTTAAGNACTCACATGACACAGTATCACTGCTTCAAACTGGGTTC 840
 DB 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATATCAATTTGCTTCCAAAATGGGTTC 834
 QY 841 TTTCTGCGCATCGAAAGTGCAGCGCTTCGCCAAAGGAGTAGTCAGAGAGCTTCTCTCAGAGC 900

Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
QY 901 AGGAAGCTAGCCAGCTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTTCTGAGGGTTTGTGTTGCTGGGCTCCA 954
QY 961 TACTGTCTGTTTCAAAATGCTTCTTCAACTTTACCCAGAGCGGAAACGCGCCAAATCGGTG 1020
Db 955 TATCTCTGTTTCAAAATGCTTCTTCAACTTTTATCTCAGCAACAGGTCCTTAATCAGTT 1014
QY 1021 TGGTACAGCATGCTCTGCTGCTGCAATGTTCAATTTGTTTGAATCCCTTCTGTAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTTCAGTGGTCAATTTCTTGTCAATCTCTTTTGTAT 1074
QY 1081 CCTTTGTGTACAGCGGTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTACAAAGCAA 1140
Db 1075 CCATTTGTGTACAGCGGTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTATTAAGCAA 1134
QY 1141 CCAGCGGTGTACAGAAAC--CAGTCAGATCTTCTTGA 1176
Db 1135 CCTCTACATCACACACAGTCGGTCAAGTATCTTCTTAA 1173

RESULT 7

ID ABZ80663 standard; cDNA; 1173 BP.

AC ABZ80663;

DT 13-JUN-2003 (first entry)

DE Human histamine receptor coding sequence.

KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
KW psoriasis; receptor.

XX Homo sapiens.

OS Key Location/Qualifiers

FH 1. 1173
FT CDS /*tag= a
FT /product= "Histamine receptor"

FT US6204017-B1.

XX 20-MAR-2001.

XX 07-OCT-1999; 99US-00414010.

XX 07-OCT-1999; 99US-00414010.

XX (SCHE) SCHERING CORP.

XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;
XX Wang S;

XX WPI; 2002-442063/47.

XX P-PSDB; ABO98629.

XX New nucleic acid encoding antigenic part of human histamine receptor,
XX useful for preparing antibodies, e.g. for treating-histamine related
XX disorders.

XX Example 1; Col 27-28; 19pp; English.

XX This sequence represents the open reading frame for a human histamine
XX receptor (HR) designated SP9144. The sequence was isolated by searching
XX databases with the sequence of known G-coupled protein receptor (GPCR).

CC The gene is used for recombinant production of HR and for preparing
CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity
CC chromatography, in immunoassay of histamine receptor, to identify cDNA
CC clones that express the receptor, as antagonist to block binding of
CC histamine (for treating any histamine-associated disorder) and to
CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR
CC protein can be used in the treatment of e.g. inflammation, asthma,
CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
CC sclerosis, inflammatory bowel disease and psoriasis

XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2.4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAAGTACTGGCATCTTGGCCAGCTGTCTAGGTCCTTGGCAATTT 60

Db 1 ATGCCAGATACATAAGCAAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

QY 61 TTAATGCTTCATTTGCTTTGCTATAATGCTAGCAATGCTGTGTCATCTTAGCCTTT 120

Db 61 TTTATGCTTCATTTGCTTTGCTATAATGCTAGCAATGCTGTGTCATCTTAGCCTTT 120

QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

QY 181 GACTTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240

Db 181 GACTTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240

QY 241 AATTTTGGAGTGGAAATCTGCAATGTTTGGCTCAATTAATTTTCTTAATTTGGCTATTTCT 300

Db 241 AATTTTGGAGTGGAAATCTGCAATGTTTGGCTCAATTAATTTTCTTAATTTGGCTATTTCT 300

QY 301 TCTCTCTACAAATATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360

Db 301 TCTCTCTACAAATATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360

QY 361 TCTTATAGGGCTCAACACACTGGGCATCATGAAGATTTGTTTGTCAAAATGGTGGCTTTGG 420

Db 361 TCTTATAGGGCTCAACACACTGGGCATCATGAAGATTTGTTTGTCAAAATGGTGGCTTTGG 420

QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGCTTCCAGATTTCTTGAAGAAGACAG 480

Db 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGCTTCCAGATTTCTTGAAGAAGACAG 480

QY 481 ACAGAACACAAAGGACTGTGAGCCTTGGCTTTGTTTACAGAGTGGTACATCTCCATTTACA 540

Db 481 ACAGAACACAAAGGACTGTGAGCCTTGGCTTTGTTTACAGAGTGGTACATCTCCATTTACA 540

QY 541 ATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACATTTAC 600

Db 541 ATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACATTTAC 600

QY 594 TCAATTTTGGAAATTCGTTGATCCCACTCATCTTAGTCTGCTTATTTTCAAGAGATTTAT 594

Db 594 TCAATTTTGGAAATTCGTTGATCCCACTCATCTTAGTCTGCTTATTTTCAAGAGATTTAT 594

QY 601 TGGAGCTGTGGAAGCGTAGGGCTTCTCAGTAGGTGCTTCCATGCTGGATTTCTTCCACT 660

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QY 654 TGGAGCTGTGGAAGCGTAGGGCTTCTCAGTAGGTGCTTCCATGCTGGATTTCTTCCACT 654

Db 654 TGGAGCTGTGGAAGCGTAGGGCTTCTCAGTAGGTGCTTCCATGCTGGATTTCTTCCACT 654

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Db 720 ACCTCTTCCAGTGTCTTCCAGGACATTTACAGAGCTGGGGTGGTGGTGGTGGTGGTGGTGG 720

QY 714 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714

Db 714 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714

QY 780 CCTGGATTGAAGGAATCAGCTGCTTCTGCTCAGTCAAGAGTCTTCCAGAGAGAGGAGC 780

Db 780 CCTGGATTGAAGGAATCAGCTGCTTCTGCTCAGTCAAGAGTCTTCCAGAGAGAGGAGC 780

QY 775 CTCAATGTTTCTTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGTTC 834

Db 775 CTCAATGTTTCTTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGTTC 834

Db 715 TCTGATCGACAGAGTCTGATCTCTTCATTCAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGACTCAGACAGAGATATCTGCTTCAAGTGGGTCC 840
Db 775 CTCATGTTTCTCAGAACCCAGATGAATAGCAATACAAATGCTTCCAAATGGTTC 834
Qy 841 TTCTGGCGATCGGAAGTGGAGCTTTCGCAAGGGAGTACGAGAGCTTCTCAGAGC 900
Db 835 TTCTCCCAATCAGATCTGTAGCTTTCACCAAGGGAGCAATGTTGAATGCTTAGAGCC 894
Qy 901 AGAAGCTAGCCAGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGCTCCA 960
Db 895 AGAGATAGCAAGTCACTGGCCATCTCTTAGGGGTTTTGCTGTTGGTGGCTCCA 954
Qy 961 TACTGTCTGTCAAAATGCTTTCAACTTACCCAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 955 TATCTCTGTTCACAAATGCTTTCATTTTATTTCTCAGCAACAGAGTCTTAAATCAGTT 1014
Qy 1021 TGGTACAGATGCTTCTGGCTCAATGGTTCAATTCGTTTGTATTCCTTCTGTAC 1080
Db 1015 TGGTATGAATGCAATTTGGCTTCAGTGGTTCAATTCCTTGTCAATCTCTTTGTAT 1074
Qy 1081 CTTTGTGTTCACAGGCGTTTCCAGAGGCTTTCGGAAGATATCTTGTGACAAAGCAA 1140
Db 1075 CCATTTGTTCACAGGCGTTTCAAGAGCTTCTTGAAATATTTGTATAAAGAGCAA 1134
Qy 1141 CCAGGCTGTTCACAGAAC---CAGTCAATCTTCTTGA 1176
Db 1135 CCTCTACATCACACAGTGGTCAATCTTCTTAA 1173

RESULT 9

AAI70980
ID AAI70980 standard; cDNA; 1173 BP.
AC AAI70980;
XX
DT 18-MAR-2002 (first entry)
DE Human histamine H4 receptor cDNA.
XX
KW Histamine H4 receptor; human; antiallergic; antiallergic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
DR P-PSDB; AAM50564.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
PS Claim 4; Fig 1; 92pp; English.
XX
XX The present sequence is that of cDNA clone pH4R encoding a human
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. The invention provides mammalian (human, mouse, rat
CC and guinea pig) histamine H4 receptor nucleic acid molecules (see

CC AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have
CC been expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the human histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy 1 ATGTCGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
Db 1 ATGCCAGATATAAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGCTTCAATTTGCTTGTCTAATGCTAGCAATGCTGTGCTCATCTTAGCCCTTT 120
Db 61 TTTATGCTTCAATTTGCTTGTCTAATGCTAGCAATGCTGTGCTCATCTTAGCCCTTT 120
Qy 121 GTGCTGGACAGAAACCTTAGACATCGAAGTAAATTTATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGCTGGACAGAAACCTTAGACATCGAAGTAAATTTATTTTCTTAATTTGGCTATTTCT 180
Qy 181 GACTTCTCTGCTGGGTTTGAATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACATGG 240
Db 181 GACTTCTCTGCTGGGTTTGAATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACATGG 240
Qy 241 AATTTTGAAGTGAATCTGATCTTTTGGCTCATCTACTGACTATCTTTTGGACCCCA 300
Db 241 GAATTTGGAAGTGAATCTGATCTTTTGGCTCATCTACTGACTATCTTTTGGACCCCA 300
Qy 301 TCTGTCTACAATATTGCTCTCATTAGCTACGATCGATACAGTCACTGATTTCAATGCTGTG 360
Db 301 TCTGTATATAACATTTGCTCTCATTAGCTACGATCGATACAGTCACTGATTTCAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAATGCTGGCTGTTTGG 420
Db 361 TCTTATAGACTCAACACTGCTGGGCTCTGAAGATTTGTTTACTCTGATGCTGGCTGTTGG 420
Qy 421 ATACTGCTTCTTGTGTAATGGCCGATGATCTGCTTCCAGATTTCTTGGAGAACAGC 480
Db 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCTAGAGTCTTGGAGAGG 476
Qy 481 ACAGAACAAAGGACTGTGAGCTGGCTTTCTTACAGAGTGGTACATCTCCACCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGATGGTACATCTTGGCCATACA 534
Qy 541 ATGCTCTTTGGAATTTCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCACTTCTAGTGGCTTATTTCAACATGAATTTAT 594
Qy 601 TGGAGCTGTGGAGCGTAGGCTCTCAGTAGTGGCTTCCCTAGCCATGCTGGATTTCTCCACT 660
Db 595 TGGAGCTGTGGAGCGTAGGCTCTCAGTAGTGGCTTCCCTAGCCATGCTGGATTTCTCCACT 654
Qy 661 ACCTCTTCCAGTGTCTTACAGGACATTTACAGAGCTGGGCTGGCTTGCAGACAGAGTAA 720
Db 655 GTCTCTTCCACATCTGTGGACATCTATTACAGAGTAGACTATCTTCAAGAGAGATCTCT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 715 TCTGATCGACAGAGTCTTCTGCAATCTTCTTATTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGGACTCACATGAACAGCAGTATCACTGCTCTCAAAGTGGGTTC 840
Db 775 CTCATGTTTCTCAGAACCCAGATGAATAGCAATACAAATGCTTCCAAATGGTTC 834


```
Db 421 GTGCTGGCCCTTTAGTGAATGGCCCAATGATCTTAGTTTCAGAGTCTTGGAAAGA----- 476
Qy 481 ACGAACAACAAGAGCTGTGAGCCCTGGCTTTGTATACAGAGTGGTATCATCTCTCACCATTAACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGGAATGGTATCATCTCTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATCTGCTTCTGCTGTCATCTCTGTGGCTTATTTCAATGATACAAATTAC 600
Db 535 TCATTTCTTGGAAATCTGCTGATCCAGTCACTCTTAGTGGCTTATTTCAACATGAATATTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGCTTCTAGTAGTGGCTTACCTAGCCATGCTGGATTTCTCCACT 660
Db 595 TGGAGCCTGTGGAAGCGTAGTCACTCTAGTAGTGGCTTACCAAGCCATCTGGAGTACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTAGGACACTTACAGAGCTGGGGTGGCTTGGAGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCACTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGCATCTGCTCACTCAGAAAGTCTCTCGAAGAAAGCAGC 780
Db 715 TCTGATCGACAGAAGTTCCTGGCATCTCTTCACTCAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTGCTCTTAAGGACTCAATGAACAGCAGTATCACTGCTTCAAAAGTGGGTTCC 840
Db 775 CTCAATGTTTCTCAAGAACCAAGATGATAGCAATCAATTTGCTTCCAAATGGGTTCC 834
Qy 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGTCTTCAACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
Qy 901 AGGAAGCTAGCAGGTCTAGTGGCCATCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCAAGTCTAGTGGCCATCTCTTAGGGGTTTTTGTGCTTGGGCTCCA 954
Qy 961 TACTGTCTGTTCACAATTTCTTCACTTACCCAGAAAGGAGCGCCCAAAATCGGTG 1020
Db 955 TATCTCTGTTCACAATTTCTTCACTTATTTCTCAGCAACAGGCTTCAATCAGTT 1014
Qy 1021 TGGTACAGATTCGCTTCTGGCTGCAATGGTTCAATCTGTTTGAATCCCTTCTGTAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGGTTCAATCTGTTGTCAATCTCTTGTAT 1074
Qy 1081 CCTTTGCTCAGAGCGTTTCCAGAGCGTTTCTGGAAGATCTTGTGTCACAAAGCAA 1140
Db 1075 CAAATGTGTCAAGCGCTTTCAAAGAGGCTTCTTGAAGAAATATTTGTATATAAAGCAA 1134
Qy 1141 CCAGGCTGTTCAGAAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACAGTCGGTCACTAGTATCTTCTTAA 1173
```

RESULT 11

ACA93262
ID ACA93262 standard; cDNA; 1173 BP.

XX ACA93262;

XX 16-JUL-2003 (first entry)

XX Human cDNA encoding GPCR hrup7.

XX Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
KW hARE-5; hrup3; hrup5; hrup6; hrup7; hGPCR27; hARE-1; hARE-2; hPR1; hG2A;
KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hrup4; signalling cascade.

XX Homo sapiens.

XX US2003017528-A1.

XX 23-JAN-2003.

XX 06-JUN-2001; 2001US-00875076.

XX 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136587P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 28-SEP-1999; 99US-0156333P.
PR 28-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.

(CHEN/) CHEN R.

(DANG/) DANG H T.

(LIAN/) LIAN C W.

(LINI/) LIN I.

Chen R, Dang HT, Lian CW, Lin I;

WPI; 2003-428952/40.

P-PSDB; ABU92265.

Novel endogenous, orphan, human G protein-coupled receptors useful for identification of modulators of the receptor and as research tools for understanding the role of the receptor in human body.

Claim 25; Page 22; 54pp; English.

The invention relates to a human G protein-coupled receptor (GPCR) appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93258-ACA93274) named hARE-3, hARE-4, hARE-5, hrup3, hrup5, hrup6, hrup7, hGPCR27, hARE-1, hARE-2, hPR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hrup4. Also included are a plasmid comprising a vector and one of the cDNAs above and a host cell comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists. In vitro and in vivo systems incorporating GPCRs is useful for elucidating and understanding the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signalling cascade. The cDNAs are useful for making a probe for dot-blot analysis against tissue mRNA and/or RT-PCR identification of the expression of the receptor in tissue samples. The present sequence is a cDNA encoding a GPCR of the invention

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 7; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2.4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCACACAGCTGCTCAGTCCCTTGGCATTT 60

Db 1 ATGCAGATACTAATAGCACATCAATTTATCACTAAGCACTCGTTACTTTAGCATTT 60

Qy 61 TTAATGCTCTCAATTTGCCCTTTCCTATAATGGTAGGCAATGCTGGTCACTTTAGCCTTT 120

Db 61 TTTATGCTCTTAGTAGTCTTTTGTATATGCTAGGAAATGCTTTGGTCATTTTAGCTTT 120

Qy 121 GTGGTGGACAGAAACCTTAGACATCGAGTATATTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGGTGGACAAACCTTAGACATCGAGTATATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCTCTGCTGGGTTTGAATTTCCATTTCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240

Db 181 GACTTCTTTGTGGGTGTGATCTCCATCTCTTTGTACATCCCTCAGACGCTGTTGGAATGG 240

Qy 241 AATTTTGGAAAGTGGAAATCTGCAATGTTTGGCTCACTACTGACTATCTTTTGCCACCGCA 300

Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy TCTCTCTACAAATATGTCCTCATAGCTACGATCGATACCACTCAGTTTCAAAATGCTGTG 360
Db 301 TCTGTATATAACATGTGCTCATCAGCTATGATGATACCTGTGCTCAGTCTCAAAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGCTGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGTAGTGGCCGTTGG 420
Qy 421 ATACTGGCTTCTTGGTAATGGCCGATGATTCCTGGCTTCAGATTCCTTGAAGAAGCAGC 480
Db 421 GTGCTGGCCCTCTTGTAGTAATGGCCCAATGATTCCTAGTTTCAGAGTCTTGGAAAGCA 476
Qy 481 ACGAAACAAAGGACTCTGTAGCCTGGCTTGTGTACAGAGTGGTACATCCTCACCATTACA 540
Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTATCCTCTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATTCCTGTCTTCTGTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTC 600
Db 535 TCATTTCTGGAATTCGTGATCCCGATCATCTTAGTCTGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTAGGCTCTCAGTAGTGGCCCTAGCCATGCTGGAATTCCTCACT 660
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGGCCAAAGCCATCCTGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGACACTTACACAGAGCTGGGTGGCTTGCAGGACAGATTAAT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CTGTGATGAAGGAATCAGCTGCTCATCTCGTCACTCAGAAAGTCTCTGAAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAAAGTCTCTGCATCTTTCATTCAGAGAGAGAGAGAGTAGT 774
Qy 781 ATCTCGTGTCTTAAGACTCATAGAACAGAGATATCATCTGCTTCAAGTGGGTTC 840
Db 775 CTCAATGTTTTCTCTCAAGAACCAAGATGAATAGCAATACAATGCTTCCAAATGGGTTC 834
Qy 841 TTCTGCGGATCGGAAGTGCAGCGCTTCCGCAAGGAGTACGACAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCTGTAGTCTTTCACCAAGGGAACATGTTGAATCTCTTAGAGCC 894
Qy 901 AGGAAGTACGCCAGTCACTGGCCATCTTCTCAGAGCTTTTGGCAATTTCTGGGTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTGTGTTGCTGGGTCCA 954
Qy 961 TACTGTCTGTACAAATGTCCTTTCAACTTACCCAGAACGGAAAGCCCAATCGGTG 1020
Db 955 TATTCTCTGTTCACAAATGTCCTTTCATTTTATTCCTCAGAACAGGTCTCTAAATCAGTT 1014
Qy 1021 TGTACAGCAATTCCTTCTGGCTGCAATGTTCAATTCGTTTGAATCCCTTCTGTAC 1080
Db 1015 TGTATAGAAATGCAATTTGGCTTCAGTGCTTCAATCTCTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
Db 1075 CCAATTGTGTACAGGCGTTTCCAAAGGCTTCTTGAAATATTTTGTATATAAAGCAA 1134
Qy 1141 CCAGCGCTGTACAGAAC--CAGTCAGTATCTCTTGA 1176
Db 1135 CCTCTACCATCAACACACAGCTGGTCAATCTCTTAA 1173

RESULT 12

ABK12959
ID ABK12959 standard; DNA; 1266 BP.

XX AC ABK12959;

XX AC ABK12959;

DT 09-APR-2002 (first entry)

DE DNA sequence of human G-protein coupled receptor TGR62 gene.

XX KW Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease; signal transduction modulator; cerebral cavernous malformation; ds; hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure; nephritis; hypertension; liver disease; cirrhosis; blood disorder; spleen-associated disorder; immune disorder; gene; chromosome 18p11.
OS Homo sapiens.
XX Key Location/Qualifiers
FT CDS 25..1195
FT /*tag= a
FT /product= "Human G-protein coupled receptor TGR62"
XX WO200200719-A2.
XX 03-JAN-2002.
XX 25-JUN-2001; 2001WO-US020363.
XX 23-JUN-2000; 2000US-0213461P.
XX (TULA-) TULARIK INC.
XX Lin DC, Zhao J, Chen J, Cutler G;
XX WPI; 2002-147880/19.
XX P-PSDB; AAU74906.
XX New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma.
XX Claim 7; Page 60-61; 78pp; English.
XX The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRs TGR62, TGR130.1, TGR130.2, human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases such as renal failure, nephritis, nephrotic syndrome, hypertension and urinary abnormalities, renal tubule defects, hypertension and nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders or conditions e.g. splenic enlargement, immune disorders, blood disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present nucleic acid sequence is that of the human GPCR TGR62 gene located on chromosome 18p11 and encodes the human GPCR TGR62 protein of the invention. This sequence encodes one of seven novel G protein coupled receptors of the invention (ABK12957- ABK12964)
XX Sequence 1266 BP; 317 A; 268 C; 242 G; 439 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1266;
Best Local Similarity 75.1%; Pred. No. 2.6e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCCCTTGGCATTTT 60
Db 25 ATGCCAGATACATAAGCAATCAATATATCAATAGCACTCGGTACTTTAGCATTT 84
Qy 61 TTAATGTCTTCAATTTGCTTTGCTATAATGGTAGCAATGCTGTGCTCATCTTAGCCTTT 120
Db 85 TTTATGTCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGTCATTTAGCTTTT 144
Qy 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTTCTTAATTTGGCTATTCT 180

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Db 145 GTGTGGACAAAACCTTAGACATCGAAGTAGTATTTTTTTCTTAATCTGGCATCTCT 204
Qy 181 GACTTCCTCGTGGGTTTGAATTCATTCCTCTGTACATCCCTACAGTGTGTTTAACTGG 240
Db 205 GACTTCCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTACACGCTGTTGGAATGG 264
Qy 241 AATTTTGAAGTGAATCTGCATGCTTTTGGCTCAATTAATGACTATCTTTTGTGCACCGCA 300
Db 265 GAATTTGGAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTGTATGTACAGCA 324
Qy 301 TCTGCTACATAATGCTCTCATTAATGCTACATCGATACCACTCAGTTCAGATTCCTGCTG 360
Db 325 TCTGTATATACATTTGCTCTCATGATATGATGATACCTGTGAGTCTCAATGCTGTG 384
Qy 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTTGTCTCAAAATGGTGGCTGTTTGG 420
Db 385 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTTGTACTCTGATGCTGGCGTGGTGG 444
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATCTTGGCTTCAGATTCCTTGAAGAACAGC 480
Db 445 GTGCTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTCAGAGTCTTGAAGAGA---- 500
Qy 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 540
Db 501 --TGAAGTAGTGAATGTAACCTGGATTTTTTTCGGAATGTGTACATCTTGGCCATACA 558
Qy 541 ATGCTCTTGGAAATTCCTGCTTCTCTGATCTCTGTGGCTTATTTTCAATGTACAGATTAC 600
Db 559 TCAITCTTGGAAATTCGTATCCCATCTATCTTAGTTCGCTTATTTTCAACATGAATATTTAT 618
Qy 601 TGGAGCCTGTGAAGCCTAGGCTCTCAGTAGGTGCTTACCACTAGCTGATTCCTCACT 660
Db 619 TGGAGCCTGTGAAGCCTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGAATGACTGCT 678
Qy 661 ACCTCTTCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTCGAGGACAAAGTAAT 720
Db 679 GTCTCTTCCACATCTGTGGACACTTATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 738
Qy 721 COTGAAATGAAGGAATCAGTCTCATCTCGTCTACTCAGAAAGTCTCGAAGAAAGACGAC 780
Db 739 TCTGCATCGACAGAAAGTCTCTGCATCTTTCATTTCAGAGAGACAGAGGAGAAAGTAGT 798
Qy 781 ATCTGTGTCTTGAAGACTCAGATCAGACAGACTATCACTGCCTTCAAGTGGGTTC 840
Db 799 CTCTATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 858
Qy 841 TTCTGGCATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCGAGAGCTTCTCAGAGGC 900
Db 859 TTCTCCCAATCAGATCTGTAGTCTTTCACCAAGGGAACATGTTGAACCTGTAGAGCC 918
Qy 901 AGGAAGCTAGCAGGTCATCTGGCCATCTCTTCTGAGCGCTTTTGGCCATTTGCTGGGTC 960
Db 919 AGGAGATAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGCTGGGCTCCA 978
Qy 961 TACTGTCTCTTCACAATCTCTTCAATCAATCCCAAGACGAGCGCCCAAAATCGGTG 1020
Db 979 TATTCCTCTTTCACAAATTTGCTTTCATTTATCTCTCAGCAACAGGTCTTAAATCAGTT 1038
Qy 1021 TGGTACAGATGCGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
Db 1039 TGGTATAGAAATTTGCAATTTGGCTTCTAGTGGTTCATTCCTTTGTCAATCCTCTTTGTAT 1098
Qy 1081 CTTTGTGTACAGGCGTTTCAGAGAGCTTCTGGAAGATCTTGTGTGCAAGCA 1140
Db 1099 CCAATGTGTACAAAGCGCTTTCAAAAGGCTTCTTGAAAATATTTTGTATAAAAAGCAA 1158
Qy 1141 CAGCGCTCTCAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1159 CTTCTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1197
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ABA02496
ID ABA02496 standard; DNA; 1300 BP.
XX
AC ABA02496;
DT
DT 26-MAR-2002 (first entry)
XX
XX Human G protein-coupled receptor nGPCR-2067-encoding DNA.
DE
XX Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;
XX signal transduction; mental disorder; central nervous system disease;
XX metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
XX psychotic disorder; Huntington's disease; schizophrenia; migraine;
XX depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
XX Parkinson's disease; proliferative disorder; cancer; psoriasis;
XX benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;
XX thyroid disorder; cardiovascular disease; hypotension; hypertension;
XX thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
XX inflammatory conditions; autoimmune disorder; rheumatoid arthritis;
XX hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
XX antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;
XX cardiant; antiatherosclerotic; neuroleptic; antimigraine;
XX antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
XX anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;
XX antipsoriatic; gene therapy; gene; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 41..1213
FT /*tag= a
FT /product= "Human nGPCR-2067"
XX
XX WO200185793-A2.
XX
XX 15-NOV-2001.
XX
XX 08-MAY-2001; 2001WO-US014750.
XX
XX 08-MAY-2000; 2000US-0203108P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Lind P, Sejlitz T, Vogeli G, Wood LS;
XX
XX WPI: 2002-062240/08.
XX
XX P-PSDB; AAM53050.
XX
XX New polynucleotide, useful for identifying modulator compounds which are
XX used for treating psoriasis, schizophrenia, diabetes, encodes the novel G
XX protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).
XX
XX Claim 4; Page 62-63; 100pp; English.
XX
XX This sequence represents a polynucleotide encoding a novel human G
XX protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCRs,
XX nGPCR-2067 has 7 putative transmembrane domains and is involved in signal
XX transduction. The invention also relates to expression vectors and host
XX cells comprising nucleic acids encoding nGPCR-2067, to recombinant
XX expression of nGPCR-2067, to antibodies specific for nGPCR-2067, to drug
XX screening methods that use nGPCR-2067, and to modulators of nGPCR-2067
XX activity. nGPCR-2067 nucleic acid sequences may be used to isolate nGPCR-
XX 2067 allelic variants and species homologues and may also be used in
XX genetic mapping. The invention also discloses the use of nGPCR-2067
XX nucleic acids in screening for a predisposition to nGPCR-2067-associated
XX hereditary mental disorders, or for the diagnosis of these disorders.
XX nGPCR-2067 nucleic acids may additionally be used to generate transgenic
XX animals, including knockout animals, which may provide an insight into
XX treating a variety of human disorders, and may also be used in the design
XX of antisense molecules for suppressing expression of nGPCR-2067 in cells.
XX nGPCR-2067, and nGPCR-2067 modulators may be used to treat a wide variety
XX of medical conditions, particularly mental disorders, central nervous
XX system diseases, and metabolic diseases. Diseases that may be treated
```

CC include viral infections, particularly HIV-1 or HIV-2 infections; pain;
CC central nervous system, neurological and psychotic disorders such as
CC Huntington's disease, schizophrenia, migraine, depression, anxiety,
CC bipolar disorder, dementia, Alzheimer's disease, and Parkinson's disease;
CC proliferative disorders such as cancers, benign prostatic hypertrophy and
CC psoriasis; metabolic disorders such as diabetes, dyslipidaemia, obesity,
CC and anorexia; thyroid disorders; cardiovascular diseases such as
CC hypotension, hypertension, thrombosis, myocardial infarction,
CC cardiomyopathies, and atherosclerosis; inflammatory conditions;
CC autoimmune disorders (e.g., rheumatoid arthritis); hormonal disorders;
CC and renal failure
XX
SQ

Query Match 58.4%; Score 686.6; DB 6; Length 1300;
Best Local Similarity 75.1%; Pred. No. 2.6e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60
DB 41 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 100
QY 61 TTAATGCTTCATTTGCTTGTCTATTAATGGTAGGCAATGCTGTGTCATCTTAGCCCTTT 120
DB 101 TTTATGTCCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 160
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
DB 161 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCCATCTCT 220
QY 181 GACTTCTCTGGGTGTGATTCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG 240
DB 221 GACTTCTCTGGGTGTGATTCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG 280
QY 241 AATTTTGGAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTTGTGCACGCA 300
DB 281 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTTTTGTGCACGCA 340
QY 301 TCTGTCTACAATATTTGCTCTCAATAGTACGATCGATACAGTCAGTCAGTTCCAAATGCTGTG 360
DB 341 TCTGTATATACATTTGCTCTCAGCTATGATCGATACCTGTGCTCAATGCTGTG 400
QY 361 TCTATAGGCTCAACACATCTGGCATCATGAAGATGTTGCTCAAAATGTTGGCTGTTGG 420
DB 401 TCTATAGAACTCAACATCTGGGGTCTTGAAGATGTTTACTCTGATGGTGGCGCTTGG 460
QY 421 ATACTGCTTCTTCTGTAATGCCCCGATGATCTGCTTCAGATCTTGGCTTGAAGAACAGC 480
DB 461 GTGCTGGCTTCTTAGTGAATGGGCCAATGATCTAGTTTTCAGAGTCTTGGAAAGGA--- 516
QY 481 ACGAACACAAAGGACTGTGAGCTGCTGCTTGTGTACAGAGTGGTACATCCTCACCATTACA 540
DB 517 --TGAAGGTAGTGAATGTGAACCTGATTTTTCGAAATGGTACATCCTTGCATCACA 574
QY 541 ATGCTCTTGAATCTCTGCTCTCTGCTCATCTCTGTGGCTTAATTTCAATGTACAGATTTAC 600
DB 575 TCATTTCTTGAATCTCTGATCCAGTCACTTAGTGTGCTTAATTTCAACATGATATTTAT 634
QY 601 TGGAGCTCTGGAGGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGATTTCTCACT 660
DB 635 TGGAGCTCTGGAGGTGATCATCTCAGTAGTGCCCAAGCCATCCTGCACTGCTGCT 694
QY 661 ACCTCTTCCAGTCTTTCAGGACATTTACACAGAGTGGGTGGCTGTCAGGCAAGTAAAT 720
DB 695 GATCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 754
QY 721 CTTGGATGAAGAAATCAGTGCATCTGCTCACTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
DB 755 TCTGCATCAGACAAAGTCTCTGCATCTTTTCAATTCAGAGACAGAGGAGAAAGATAGT 814
QY 781 ATCTGCTGCTCTTAAAGGACTCATGAACAGCAGTATCACTGCTCTCAAGTGGGTCC 840
DB 815 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGCGTTCC 874

QY 841 TTCTGGCATCGAAGTGCAGCCCTTCGCCAAGGGAGTAGCGAGAGCTTCTCAGAGGC 900
DB 875 TTCTCCCAATCAGATTTCTGTAGCTCTTTCACCAAGGGAACATGTTGAATCTGTTAGAGCC 934
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGCTCCA 960
DB 935 AGGAGATTAGCCAGTCACTGGCCATCTTCTAGGGGTTTTTGTGTTGCTGGGCTCCA 994
QY 961 TACTGTCTGTCAATTTGCTTTCCTTCACTTACCCAGAACGGAACGCCCAATTCGGTG 1020
DB 995 TATTCTCTGTTCACAATTTGCTTTCATTTATTTCTCAGCAACAGCTCCTAATCAGTT 1054
QY 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGTTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
DB 1055 TGGTATAGAAATTCATTTTGGCTTTCAGTGTTCATTTCTTGTCAATCTCTTTTGTAT 1114
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
DB 1115 CCATTTGTGTACAGGCGTTTCAAGGCTTCTTGAATAATTTTGTATAAAAGCAA 1174
QY 1141 CCAGCGCTGTCAAGAAC---CAGTCAAGTATCTTCTTGA 1176
DB 1175 CCTCTACCATCAACACACAGTCGTCAGTATCTTCTTAA 1213
RESULT 14
AAH47911
ID AAH47911 standard; cDNA; 1312 BP.
XX
AC AAH47911;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human G protein-coupled receptor protein BG26 encoding cDNA.
XX
KW Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
KW altering intracellular cAMP concentration;
KW regulating signal transduction; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 64..1236
FT /*tag= a
FT /product= "G protein-coupled receptor BG26"
XX
PN WO200146414-A1.
XX
PD 28-JUN-2001.
XX
PF 20-DEC-2000; 2000WO-JP009038.
XX
PR 20-DEC-1999; 99JP-00361687.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Itadani H, Nakamura T, Tanaka K, Ohta M;
XX
DR WPI; 2001-441675/47.
DR P-PSDB; AAG64477.
XX
PT G protein-coupled receptor protein BG26, with activity of binding to
PT histamine and capable of changing intracellular cAMP concentration in
PT response to its stimulus, applicable as tool in screening ligands or drug
PT candidates.
XX
PS Claim 1; Page 37-41; 50pp; Japanese.
XX
CC The present sequence is that of the human G protein-coupled receptor
CC protein BG26 encoding cDNA, which shows significant homology with
CC histamine H3, with activity of binding to histamine and capable of
CC changing intracellular cAMP concentration in response to its stimulus.

presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 3689 BP; 975 A; 739 C; 746 G; 1229 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 7; Length 3689;
Best Local Similarity 75.1%; Pred. No. 4.6e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY	1	ATGTCGAGTCTAACAGTACTGGCACTCTGCCACCAAGCTGCTCAGGTCCTGGCATTTT	60
Db	101	ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT	160
QY	61	TTAATGTCTTTCATTTGGCTTTGTCTATATGCTAGGCAATCTGTCGTCATCTTAGCCCTTT	120
Db	161	TTTATGTCTTGTAGTCTTTTGTCTATATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT	220
QY	121	GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTCTTAATTTGGCTATTTCT	180
Db	221	GTGGTGACAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATTTGGCCATCTCT	280
QY	181	GACTTCCTGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAAGTGTTGTTAACTGG	240
Db	281	GACTTCCTGTGGTGTGATCTCCATTCCTTTGTACATCCCTCAACGCTGTTTCGAATGG	340
QY	241	AATTTTGGAAAGTGAATCTCAGTGTGTTGGCTCATTTACTGACTATCTTTTGTGACCGCA	300
Db	341	GAITTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA	400
QY	301	TCGTCTACAATATTTGCTCTCATTAGCTACGATCGATACCAGTCAGTTTCAAAATGCTGTG	360
Db	401	TCGTATATAACATTTGCTCTCATCAGTATGATCGATACCTGTCACTCTCAAAATGCTGTG	460
QY	361	TCATTATAGGCTCAACACACTGGCATCATGAAGTTGTTGCTCAAAATGGTGGCTGTTGG	420
Db	461	TCATTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTGG	520
QY	421	ATACTGGCTTTCTTGGTAATGSCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGACAGC	480
Db	521	GTGCTGGCTTTCTTGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA	540
QY	481	ACGAACACAAAGACTCTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACATTACA	540
Db	577	--TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTGCCATCACA	634
QY	541	ATGCTCTTGGAAATCTGCTTCTGTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC	600
Db	635	TCATTCTTGGAAATCTGTATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT	694
QY	601	TGGAGCTGTGGAGGTAGGGCTCTCAGTGTGCTGCTAGCCATCGCTGGATTTCTCCACT	660
Db	695	TGGAGCTGTGGAGGCTGATCATCTCAGTGTGCTGCAAGCCATCTCGACTGACTGCT	754
QY	661	ACCTCTTCCAGTCTCTCAGGACATTTACACAGAGCTGGGGTGGCTTGCAGGACAGTAAT	720
Db	755	GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	814
QY	721	CTGTGAATGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGACAGC	780

Db	815	TCCTCATCGACAGAAAGTTTCCTGCATCCTTTTCATTTCAGAGACACAGAGAGAAAGTAGT	874
QY	781	ATCCTGTGTCTCTTAAAGACTCACAATGAACAGCAGTATCATCTGCTTCAAAAGTGGTTCC	840
Db	875	CTCATGTTTTCCTCAAGAACCAAGATGAATAGCAATCAATTGCTTCCAAAATGGTTCC	934
QY	841	TTCTGGCGATCGGAAAGTGGCAGGCTTTCGCCAAGGGAGTACGACAGACTTCTCAGAGGC	900
Db	935	TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAGGGGAACATGTTGAACCTGCTTAGAGCC	994
QY	901	AGGAAGCTAGCCAGGTCACCTGGCCATCCTTCTTCAGCGCTTTTGGCAATTTGCTGGGCTCCA	960
Db	995	AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTCTGCTGGGCTCCA	1054
QY	961	TACTGCTCTTTCACAATTTGCTTTCACCTTACCCAGAACGGAAACGCCCAAAATCGGTG	1020
Db	1055	TATTCTCTGTTCAAAATTTGCTCTTCAATTTTATTCCTCAGCAACAGGCTCTTAATCAGTT	1114
QY	1021	TGGTACAGCATTTGCTTCTGCTGCAATGTTCAATTCGTTTGTAAATCCCTTTCTCTAC	1080
Db	1115	TGGTATGAATTTGCAATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTTGTAT	1174
QY	1081	CCTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGACAAAGCAA	1140
Db	1175	CCATTGTGTCAAGGCGTTTCAAAAGGCTTTCTTGAANAATATTTTGTATATAAAGCAA	1234
QY	1141	CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA	1176
Db	1235	CCTCTACCATCACAAACACAGTCGGTCAGTATCTTCTTAA	1273

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Job time : 568 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 11:13:04 ; Search time 110 seconds
(without alignments)
5932.930 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atgtcggagcttaacagctac.....accagtcagtatcttttga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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3: /cgn2_6/prodata/2/ina/6A COMB.seq.*

4: /cgn2_6/prodata/2/ina/6B COMB.seq.*

5: /cgn2_6/prodata/2/ina/PTUS COMB.seq.*

6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686.6	58.4	1173	US-09-414-010-1	Sequence 1, Appli
2	686.6	58.4	1173	US-09-812-216-1	Sequence 1, Appli
3	143.2	12.2	1338	US-09-165-543-6	Sequence 6, Appli
4	143.2	12.2	3244	US-09-165-543-4	Sequence 4, Appli
5	140.4	11.9	1335	US-08-985-090-3	Sequence 3, Appli
6	140.4	11.9	1335	US-09-165-543-3	Sequence 3, Appli
7	140.4	11.9	1335	US-09-167-354-6	Sequence 6, Appli
8	140.4	11.9	1335	US-09-642-855-6	Sequence 6, Appli
9	140.4	11.9	1335	US-09-642-514-6	Sequence 6, Appli
10	140.4	11.9	2689	US-08-985-090-1	Sequence 1, Appli
11	140.4	11.9	2689	US-09-165-543-1	Sequence 1, Appli
12	140.4	11.9	2699	US-09-167-354-5	Sequence 5, Appli
13	140.4	11.9	2699	US-09-642-855-5	Sequence 5, Appli
14	140.4	11.9	2699	US-09-642-514-5	Sequence 5, Appli
15	94	8.0	1086	US-08-985-090-6	Sequence 6, Appli
16	94	8.0	1086	US-09-165-543-33	Sequence 33, Appli
17	94	8.0	2218	US-08-985-090-4	Sequence 4, Appli
18	94	8.0	2218	US-09-165-543-31	Sequence 31, Appli
19	93.8	8.0	1056	US-09-524-162-1	Sequence 1, Appli
20	67.6	5.7	2210	US-09-016-434-1177	Sequence 1177, Ap
21	64.4	5.5	2261	US-09-016-434-1176	Sequence 1176, Ap
22	61.2	5.2	1233	US-09-721-870-176	Sequence 176, App
23	59	5.0	1913	US-09-016-434-1314	Sequence 1314, Ap
24	57.6	4.9	1579	US-09-016-434-1243	Sequence 1243, Ap
25	56.8	4.8	2595	US-09-016-434-1178	Sequence 1178, Ap
26	56	4.8	1386	US-09-016-434-1339	Sequence 1339, Ap
27	56	4.8	1581	US-08-313-553-8	Sequence 8, Appli

28	56	4.8	1581	3	US-08-767-993-8	Sequence 8, Appli
29	56	4.8	1956	1	US-08-313-553-6	Sequence 6, Appli
30	56	4.8	1956	3	US-08-767-993-6	Sequence 6, Appli
31	55.2	4.7	1742	4	US-09-016-434-1411	Sequence 1411, Ap
32	53.6	4.6	4008	4	US-09-976-594-158	Sequence 158, App
33	51.6	4.4	1506	4	US-09-016-434-1170	Sequence 1170, Ap
34	51.6	4.4	1645	2	US-08-461-812-1	Sequence 1, Appli
35	51.6	4.4	1645	4	US-09-371-705-1	Sequence 1, Appli
36	49.4	4.2	7218	1	US-08-232-463-14	Sequence 14, Appli
37	49.2	4.2	1046	3	US-08-875-540-2	Sequence 2, Appli
38	49.2	4.2	1046	4	US-09-171-456-2	Sequence 2, Appli
39	49.2	4.2	1046	4	US-09-473-634-2	Sequence 2, Appli
40	49.2	4.2	1080	2	US-08-103-170-1	Sequence 1, Appli
41	49.2	4.2	1080	3	US-08-875-540-14	Sequence 14, Appli
42	49.2	4.2	1080	4	US-09-473-634-14	Sequence 14, Appli
43	49.2	4.2	1191	4	US-09-171-456-18	Sequence 18, Appli
44	49.2	4.2	1191	4	US-09-016-434-1217	Sequence 1217, Ap
45	48.4	4.1	1239	1	US-08-349-696-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-09-414-010-1

; Sequence 1, Application US/09414010

; Patent No. 6204017

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monsma, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

; APPLICANT: Wang, Suke

; TITLE OF INVENTION: Histamine receptor

; FILE REFERENCE: CN01069

; CURRENT APPLICATION NUMBER: US/09/414,010

; CURRENT FILING DATE: 1999-10-07

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-414-010-1

Query Match	58.4%	Score	686.6	DB	3	Length	1173
Best Local Similarity	75.1%	Pred. No.	2.9e-208				
Matches	886	Conservative	0	Mismatches	284	Indels	9
Gaps	2						
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QY	1	ATGTCGGAGCTTAACAGTACTGGCATCTTGGCCACGAGCTGCTCAGGTCCTCCCTTGGCATTT	60				
DB	1	ATGCCAGATCTAATAGCACATCAATTTATCCTAAGCACTCGTGTTACTTTAGCATTT	60				
<hr/>							
QY	61	TTAATGCTTCTATTGCTTTCCTTCTATATAGTAGGAATGCTGCTGCTCATCTAGCTTTT	120				
DB	61	TTATGCTCTAGTACTTTGCTATAAGTCTAGGAATGCTTGGTCACTTTTAGCATTT	120				
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QY	121	GTGGTGGGACAGAAACCTTADACATCGAAGTAATATTTTCTTAACTTGGCTATTCT	180				
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QY	181	GACTTCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACTGG	240				
DB	181	GACTTCTTGTGGGTGTCATCTCCATTCCTTTGTACATCCCTCACACGCTGTTGAATGG	240				
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QY	241	AATTTTGAAGTGAATCTGATGTTTGGCTCATCTAGCTATCTTTTGTGACCGCA	300				
DB	241	GATTTTGAAGGAAATCTGTGTTTGGCTCACTACTGACTATCTGTTATGTACAGCA	300				
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QY	301	TCTGTCTACAATATTGCTCTCATTAGCTACCATGATACAGTCACTTCAATGCTGTG	360				
DB	301	TCTGTCTACAATATTGCTCTCATTAGCTACCATGATACAGTCACTTCAATGCTGTG	360				

301	TCTGTATATAAACATTGCTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG	360
Db		
361	TCTTATAGGCTCAACACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG	420
Qy		
361	TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGSGTGGCCGTTGG	420
Db		
421	ATACTGGCTTTCTTGGTAAATGSCCGATGATTTCTGGCTTCAGATTCTTGGAGAACACGC	480
Qy		
421	GTGCTGGCTTCTTAGTGAATGGCCAAATGATTCTAGTTTTCAGAGTCTTGGGAAGGA---	476
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481	ACGAACACAAGACTGTGTAGCTGGCTTTGTTTACAGAGTGGTACATCTCCACATTACA	540
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477	--TGAAGTAGTGAATGTGAACCTGGATTTTTTCGGAATGGTACATCTTGGCATCACA	534
Db		
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Qy		
535	TCATTCTTGGNAATTCGTGATCCCGATCATCTTAGTCGCTTATTTCAACATGAATATTTAT	594
Db		
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Db		
661	ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTCCAGGACAAGTAAT	720
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Qy		
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Db		
781	ATCCGTGTGTCTTTAAGGACTCACATCAAAGCAGAGTATCACTGCTTCAAGTGGGTCTCC	840
Qy		
775	CTCATGTTTTCTCTCAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATTGGGTCTCC	834
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Qy		
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Db		
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Qy		
895	AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGCTGTTTCTCGGGCTCCA	954
Db		
961	TACTGTCTGTTTCAAAATGTCTTTCAACTTACCCACAGAACGGAAACGCCCAAAATCGGTG	1020
Qy		
955	TATTCTCTGTTTCAAAATGTGTCCTTTCAATTTATTTCTCTCAGCAACAGGTCTCTAAATCAGTT	1014
Db		
1021	TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTATATCCCTTCTGTAC	1080
Qy		
1015	TGGTATAGAAATGCAATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAAATCTCTTTGTAT	1074
Db		
1081	CCTTTGTCTCAGCGGTTTCCAGAAGCTTCTTGAAGATACATTTCTGTGACAAAGCAA	1140
Qy		
1075	CAATTGTGTCAAGCGCTTTCAAAAGGCTTCTTGAATAATTTTCTATATAAAAGCAA	1134
Db		
1141	CCAGCGCTGCACGAAC---CAGTCAGTATCTTCTTGA	1176
Qy		
1135	CCTCTTACCATCACAAACAGTCGGTCAGTATCTTCTTAA	1173
Db		

661	ACCTCTCCAGTGTCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT	720
Db		714
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721	CCTGGATTGAAGGAATACGTGTGCATCTCGTACTCAGAAAGTCTCTCGAAGAAGGACGC	780
Qy		
715	TCTGCATCGACAGAAGTTCTCGCATCTTCTTCAATCAGACAGACAGAGGAGAAGAGTAGT	774
Db		
781	ATCCTGGGTGTCCTTAAGAGACTCACATGAACAGCAGTATCACTCGCCTTCAAAGTGGGTTC	840
Qy		
775	CTCATGTTTTCTCTCAAGAACCAAGATGATAGCAATACAAATTGCTTCCAAATGGGTTC	834
Db		
841	TTCTCGCATCGGAAGTGCAGGGCTTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC	900
Qy		

RESULT 2
US-09-812-216-1
/ Sequence 1, Application US/09812216
/ Patent No. 6613533
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Jiang Xu
/ APPLICANT: Hedrick, Joseph A.
/ APPLICANT: Laz, Thomas M.
/ APPLICANT: Monmsa, Frederick J. Jr.
/ APPLICANT: Morse, Kelley L.
/ APPLICANT: Umland, Shelby P.
/ APPLICANT: Wang, Suke
/ TITLE OF INVENTION: Histamine receptor
/ FILE REFERENCE: CWC1069

Db 835 TTTCTCCCAATCAGATCTCTAGTCTTTCCACAAAGGGAACATGTTGAATGCTTAGAGCC 894
QY 901 AGAAGCTAGCCAGTCACTGGCCATCCTTCTGAGCGCTTTTGGCAATTTGCTGGGTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGGCTTTTGGCTGGGTCCA 954
QY 961 TACTGTCTCTTCCAAATTTGCTTTTCAACTTACCCAGAAAGGAGCGCCCAATCGGTG 1020
Db 955 TATTCTCTGTTCAATTTGCTTTTCAATTTTATCTCTCAGCAAGGTCTTAATCAGTT 1014
QY 1021 TGGTACAGATTGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Db 1015 TGGTATAGAAATTGCAATTTGGCTTCACTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT 1074
QY 1081 CTTTGTGTGTCAGAGGCTTTCAGAAAGGCTTTCTGGAAGATCTTTGTGTGCAAGGAA 1140
Db 1075 CCAATTTGTGTCAGAGGCTTTTCAAAAGGCTTTCTTGAAATATTTTGTATAAAAAGCAA 1134
QY 1141 CCAGCGCTCTGCAGAAC--CAGTCAGTATCTTCTTGA 1176
Db 1135 CTTCTACCATCAACACAGTGGTCTGATCTTCTTAA 1173

RESULT 3

US-09-165-543-6
; Sequence 6, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335

US-09-165-543-6

Query Match 12.2%; Score 143.2; DB 3; Length 1338;
Best Local Similarity 54.2%; Pred. No. 3e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 3 GTCCGAGTCTAAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCCTTGSCATTTTT 62
Db 60 GCGCGCTGACAGCGGGGCGCGCGCTTCTCGGCTGCTCGACCGCTGTCTCGCTGGCT 119
QY 63 AATGTCTTCAATTTGCCCTTTGCTTATATGTTAGGCAATGCTGTGGTCACTCTTACGCTTTGT 122
Db 120 CATGGGCTGCTCATCTGTGGCCACAGTACTGGGCAAGCGCTGGTCACTGCTGCCCTTGT 179
QY 123 GTTGACAGAAAACCTTGTAGACATCGAAGTAATTAATTTTCTTAAATTTGGCTATTTCTGA 182
Db 180 GCGGATTCAGAGCTCGGACCAAGAACTTCTTCTGTCTCAACTCGCCATCTCCGA 239
QY 183 CTTCTCTCTGGGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTTAAAC---TG 239
Db 240 CTTCTCTGGGTTGCTTCTGATCCCATTTGTACGTAACCTATGTCTGACCGCGGTTG 299
QY 240 GAATTTTGAAGTGAATCTGATGTTTTGGGCTCAATCTAGCTACTATCTTTTGTGACCGC 299
Db 300 GACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGGTGTAGACTTACTCTGTGTGCTC 359
QY 300 ATCTGTCTACAAATTTGCTCTCAATTAGCTACGATCGATACCACTCAGTTTCAAACTGCT 359
Db 360 CTCGGTCTTCAACATCGTACTCATCAGCTATGACCGAATTCCTGTGCTCAGTCACTCGAGCT 419
QY 360 GTCTTATAGGCTCAACACATCGGATCATGAAGATTGTGTCTCAAAATGGTGGCTGTTG 419
Db 420 CTCCTACAGGGGCGGCGGAGACACAGAGCGGGCGCTTCGGAAGATGGCACTGGTGTG 479
QY 420 GATCTGCTCTTCTTGGTAAATGGCGCGATGATCTGCTTCAGAA-----TCTTTGGAA 473
Db 480 GGTGTGCGCTTCTCTGCTGTATGGGCTTGCCTCTGAGTTGGGAGTACTCTGTGTGGTG 539
QY 474 GAACAGCAGCAACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCAC 533
Db 540 CAGTTTCCATCCCGAGGGGCACTGTATGCTGAGTTCTTCTACAACTGGTACTTTCTCAT 599
QY 534 CATTACAATGCTTGGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
Db 600 CAGGCGCTCCACCTCGAGTTCTTCCAGCGCTTCTCAGCGTTTACCTTCTTCAACCTCAG 659
QY 594 GATTTACTGGAGCCTGTGGAAGCTA 619
Db 660 CATCTACTGACATCCAGAGCGCA 685

RESULT 4

US-09-165-543-4
; Sequence 4, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 778..2112
US-09-165-543-4

Query Match 12.2%; Score 143.2; DB 3; Length 3244;
Best Local Similarity 54.2%; Pred. No. 5.1e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;
QY 3 GTGGAGTCTAACAGTACTGGCATCTTGGCCACCAAGTGTCTCAGTCCCTTGGCATTTT 62
DB 837 GCGGCTGACGGGGGGGGGGCTTCTGGCTGCTGGACCGCTGTCTGGCTGGCT 896
QY 63 AATGCTTTCATTTGCCCTTGTATTAAGTAGGCAATGCTGTGTCATCTTAGCCTTGT 122
DB 897 CATGGCCTGCTCATCTGTCGACAGTACTGGGACCGCGCTGTGTCATGCTCGCCTTGT 956
QY 123 GTGGACAGAACTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182
DB 957 GCGGATTCGAGCTTCGACCCAGAACACTTCTTCTGCTCAACCTCGCATCTCGGA 1016
QY 183 CTTCCTCGTGGGTTGATTTCCATTCCTCTGTACATCCCTCACTGTGTTTAAAC---TG 239
DB 1017 CTTCCTCGTGGTCCCTTCTGCATCCCATTTGACGTACCCCTATGTGCTGACCGCGCTG 1076
QY 240 GAATTTTGGAGTGGATCTGCATGTTTGGCTCACTACTGACTATCTTTTGTGACCGC 299
DB 1077 GACCTTCGCGGGGGCTCTGCAAGCTGTGGCTGGTAGACTACCTACTGTGCGCTC 1136
QY 300 ATCTGTCTACAATATGTCCTATTAGCTACGATCGATACCAAGTCAGTTTCAAATGCTGT 359
DB 1137 CTCGGTCTTCAAGATCGTACTATCAGTATGACGGAATTCCTGTCACTCATCGAGCTGT 1196
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGTGTG 419
DB 1197 CTCCTACAGGCGCCAGCAGGGGGACACGAGACGGCGCTTCGGAAGATGGCACTGGTGTG 1256
QY 420 GATCTGGCTTCTTGTGAATGGCCGATGATTTGCTTCAG---TTCTTGAA 473
DB 1257 GGTGCTGGCTTCTGCTGTATGGCCCTGCCATCTGAGTTGGAGTACCTGTCTGGTGG 1316
QY 474 GAACAGCAGAACACAAAGGACTGTGACCTGGCTTTGTACAGAGTGGTACATCTCAC 533
DB 1317 CAGTTCCATCCCGAGGGCAGTGTGATGCTGAGTTCTTCTACACTGGTACTTCTCAT 1376
QY 534 CATTAACATGCTCTTGGAAATTCCTGCTTCCTGTCACTCTCTGTGGCTTATTTCAATGACA 593
DB 1377 CACGGCTCCACCTCGAGTTCTTCAGCCCTTCTCAGCGCTTACCTTCTTCAACCTCAG 1436
QY 594 GATTACTGGAGCTGTGGAGCGTA 619
DB 1437 CATCTACTGAACATCCAGAGCGCA 1462

RESULT 5
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1335
US-08-985-090-3

Query Match 11.9%; Score 140.4; DB 2; Length 1335;
Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
QY 3 GTCCGAGTCTAACAGTACTGGCATCTTGGCCACCAAGTGTCTCAGTCCCTTGGCATTTT 62
DB 60 GCGGCGGGGGGGGGGGCTTCTGGCAGCTGGACCGGGTGTGGCGCGCT 119
QY 63 AATGCTTTCATTTGCCCTTGTATTAAGTAGGCAATGCTGTGTCATCTTAGCCTTGT 122
DB 120 CATGGCCTGCTCATCTGTCGACAGTGTGGCAGCGCTGTGTCATGCTCGCTTGT 179
QY 123 GTTCGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182
DB 180 GCGGAGCTCGAGCTTCGACCCAGAACACTTCTTCTGTCTCAACCTCGCATCTCGA 239
QY 183 CTTCCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCTGTG---TTTAACTG 239
DB 240 CTTCCTCGTGGCGCTTCTGCATCCCACTGTATGTACCTACGTGTGACAGCGCGCTG 299
QY 240 GAATTTTGGAGTGGAAATCTGCATGTTTGGCTCACTACTGACTATCTTTTGTGACCGC 299
DB 300 GACCTTCGCGCGGGCTCTGCAAGCTGTGGTAGTGAGTACCTGTGTGCACTC 359
QY 300 ATCTGTCTACAATATGTCCTCATTAGCTAGCTGATACCAAGTGTGTTTCAAATGCTGT 359
DB 360 CTCTGCTTCAACATCGTGTCTATCAGCTACGACGCTTCTGTGCTGTCACCCGAGCGGT 419
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGTGTG 419
DB 420 CTCATACCGGCGCCAGCAGGGGTGACACGCGGGGCGAGTGGCGAAGATGCTGTGTTG 479
QY 420 GATCTGGCTTCTTGTGGTAATGGCCCATGATCTGCTTCAGAT-----TCITGGAA 473

Db 480 GGTGCTGGCTTCTGCTGTACGGACAGCCATCTGAGCTGGGAGTACCTGTCGGGGG 539
QY 474 GAACAGACAGACACAAAGAGACTGTGAGCTGGCTTTGTGTACAGAGTGGTACATCTCTAC 533
Db 540 CAGTCCATCCCGAGGAGCCACTGTATGCGGAGTTCTTCTACAACTGGTACTTCTCTCAT 599
QY 534 CATTACAAATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGTGGCTTATTTCAATGTACA 593
Db 600 CACGGCTTCCACCTTGAGTCTTACGCGCTTCTCAGCGTACCTTCTTTAACCTCAG 659
QY 594 GATTACTGAGCTGTGGAGCGTAGGGCTCTCAG 629
Db 660 CATCTACCTGAACATCCAGAGGCGCACCCGCTCCG 695

RESULT 6
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
US-09-165-543-3

Query Match 11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
QY 3 GTGCGAGTCTAACAGTACTGGCATCTTGGCACAGCTGTCCAGTCCCTTGGCAATTTT 62
Db 60 GCGCGCGGCGGCGCGGCGGCTTCTCGGAGCTGACCGCGGTCTGCGCGCGT 119
QY 63 AATGCTTTCATTTGGCTTTGTCTATATGTTAGGCAATGCTGTGGTCACTTAGCCCTTGT 122
Db 120 CATGGCGTGTCTCATGTGGCCACGCTGTGGGCAACGCGGTGGTCTGCTGCCTTCGT 179

QY 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAAATTTGGCTATTTCTGA 182
Db 180 GGGCGACTCGAGCTCCGCGACCCAGAAACAACCTTCTTCTGCTCAACCTCGCACTCGGA 239
QY 183 CTTCTCTGCTGGGTTTGATTTTCCATTTCCATCTCTGTATACATCCCTCAGGTGTG---TTTAACTG 239
Db 240 CTTCTCTGCTGGGCGCTTCTGCACTCCACCTGTATGTATCCCTAGCTGTGACAGCGCGCTG 299
QY 240 GAATTTTGGAGTGGAAATCTGCAATGTTTTTGGCTCAITTAATCTGACTATCTTTTGTGCACGCG 299
Db 300 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGTAGTGGACTACTCTGCTGTGCACCTC 359
QY 300 ATCTGTCTACAATATGTCTCTCAITTAGCTAGATAGATACAGTCACTGTTTCAAAATGCTGT 359
Db 360 CTTGCGCTTCAACATCGTCTCATCACTAGTACGACCGCTTCTGTCGCTCACCAGCGGT 419
QY 360 GTCTTATAGGGCTCAACACACTGSCATCAAGAAGATTGTTGCTCAATGCTGCTGCTTTG 419
Db 420 CTATACCGGCGCCAGCGGGTGACAGCGCGGCGAGTGGGAAGATGCTGTGGTGTG 479
QY 420 GATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTTCAGAT-----TCTTGGAA 473
Db 480 GGTGCTGGCCTTCTCTGTGACGACCGACCATCTGAGCTGGGAGTACCTGTCCGCGGG 539
QY 474 GAACAGACAGACACAAAGAGACTGTGAGCTGGCTTTGTGTACAGAGTGGTACATCTCTAC 533
Db 540 CAGCTCCATCCCGAGGCGCACCTGTATGCGGAGTTCTTCTACAACTGGTACTTCTCTCAT 599
QY 534 CATTACAAATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACA 593
Db 600 CACGGCTTCCACCTGAGTCTTCTAGGCGCTTCTCAGGTCACCTTCTTTAACTCAG 659
QY 594 GATTACTGAGCTGTGGAGCGTAGGGCTCTCAG 629
Db 660 CATCTACCTGAACATCCAGAGGCGCACCCGCTCCG 695

RESULT 7
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-6

Query Match 11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
QY 3 GTGCGAGTCTAACAGTACTGGCATCTTGGCACAGCTGTCCAGTCCCTTGGCAATTTT 62
Db 60 GCGCGCGGCGGCGGCGGCGGCTTCTCGGAGCTGACCGCGGTCTGCGCGCGT 119
QY 63 AATGCTTTCATTTGGCTTTGTCTATATGTTAGGCAATGCTGTGGTCACTTAGCCCTTGT 122
Db 120 CATGGCGTGTCTCATGTGGCCACGCTGTGGGCAACGCGGTGGTCTGCTGCCTTCGT 179

123 GTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCTGA 182
180 GGCGGACTCGAGCCTCGCGACCCAGAGAACTTCTCTGCTCAACCTCGGCATCTCCGA 239
183 CTTCTCGTGGGTTTGATTTCCATTTCTCTGTATACCTCCCTCACGTTG---TTAACTG 239
240 CTTCTCGTGGGCTTCTGATCCACCTGATGTATACCTACGCTGTGACAGCCGCTG 299
240 GAATTTTGAAGTGAATCTGATGTTTGGCTCAATCTAGCTATCTTTTGTGACAGGC 299
300 GACCTTCGGCGGGCCTCTGCAAGCTGTGCTGTAGTGGACTACCTGTGTGACCTC 359
300 ATCTGTCTCAAAATTTCTCATTTAGCTAGATCGATACCAAGTCAGTTTCAAAATGCTGT 359
360 CTCTGCTTCAACATCTGCTCATAGCTAGCAGCGCTTCTCTGCGGTCAACCGAGCGT 419
360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGTTGGCTGTTG 419
420 CTCTACCGGGCCAGAGGTGACACGGCGGGCAGTGGGAAGATGCTGCTGTTG 479
420 GATACGCTTCTTGTGAATGCGCCGATGATTTCTGGCTTCAGAT-----TCTTGGAA 473
480 GGTGCTGGCCTTCTGCTGTAGTGGACCAAGCATCTGAGCTGGAGTACCTGTCCGGGG 539
474 GAAACAGCAGAACACAAAGGACTGTGAGCTGGCTTGTGTACAGAGTGGTATCCTCAC 533
540 CAGCTCCATCCCGAGGGCCACTGTATGCGAGTTCTTCTACAACTGGTACTTCTCAT 599
534 CATTACAAATGCTCTTGGAAATCTGCTTCTCTCATCTCTGCTGCTTCAATGTACA 593
600 CACGGCTTCCACCTGGAGTTCTTACGCCCTTCTCAGCGTCACTTCTTTAACCTCAG 659
594 GATTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
660 CATCTACCTGAACATCCAGAGCGCACCGGCTCGG 695

RESULT 8

US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlender, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-855-6

Query Match 11.9%; Score 140.4; DB 4; Length 1335;
Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
3 GTGCGAGTCTAACAGTACTGGCATTTGCCACAGCTGTCTCAGTCCCTTGGCATTTT 62
60 GCGCGCGGGCGGGCGGGCTTCTCGGAGCTGGACCGCGGTCTGCGCGCT 119
63 AATGCTCTATTGCTTGTCTATAATGGTAGGCAATGCTGTGGTCACTTAGCCTTTGT 122

120 CATGGCGCTGCTCATCTGGCCACGGTGTGGGCAACGCGTGTCTCATGCTCGCTTGGT 179
123 GTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCTGA 182
180 GGCGGACTCGAGCCTCGCGACCCAGAGAACTTCTCTGCTCAACCTCGGCATCTCCGA 239
183 CTTCTCGTGGGTTTGATTTCCATTTCTCTGTATACCTCCCTCACGTTG---TTAACTG 239
240 CTTCTCGTGGGCTTCTGATCCACCTGATGTATACCTACGCTGTGACAGCCGCTG 299
240 GAATTTTGAAGTGAATCTGATGTTTGGCTCAATCTAGCTATCTTTTGTGACAGGC 299
300 GACCTTCGGCGGGCCTCTGCAAGCTGTGCTGTAGTGGACTACCTGTGTGACCTC 359
300 ATCTGTCTCAAAATTTCTCATTTAGCTAGATCGATACCAAGTCAGTTTCAAAATGCTGT 359
360 CTCTGCTTCAACATCTGCTCATAGCTAGCAGCGCTTCTCTGCGGTCAACCGAGCGT 419
360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGTTGGCTGTTG 419
420 CTCTACCGGGCCAGAGGTGACACGGCGGGCAGTGGGAAGATGCTGCTGTTG 479
420 GATACGCTTCTTGTGAATGCGCCGATGATTTCTGGCTTCAGAT-----TCTTGGAA 473
480 GGTGCTGGCCTTCTGCTGTAGTGGACCAAGCATCTGAGCTGGAGTACCTGTCCGGGG 539
474 GAAACAGCAGAACACAAAGGACTGTGAGCTGGCTTGTGTACAGAGTGGTATCCTCAC 533
540 CAGCTCCATCCCGAGGGCCACTGTATGCGAGTTCTTCTACAACTGGTACTTCTCAT 599
534 CATTACAAATGCTCTTGGAAATCTGCTTCTCTCATCTCTGCTGCTTCAATGTACA 593
600 CACGGCTTCCACCTGGAGTTCTTACGCCCTTCTCAGCGTCACTTCTTTAACCTCAG 659
594 GATTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
660 CATCTACCTGAACATCCAGAGCGCACCGGCTCGG 695

RESULT 9

US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlender, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

Query Match 11.9%; Score 140.4; DB 4; Length 1335;
Best Local Similarity 53.6%; Pred. No. 2.3e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;
3 GTGCGAGTCTAACAGTACTGGCATTTGCCACAGCTGTCTCAGTCCCTTGGCATTTT 62
60 GCGCGCGGGCGGGCGGGCTTCTCGGAGCTGGACCGCGGTCTGCGCGCT 119

QY 63 AATGCTTCAATTTGCTTGTCTATAATGCTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122
|||
Db 120 CATGGCGTGTCTCATGCTGGCCACGCTGTGGCAACGCGTGTGTCTCATGCTGCTTGT 179
QY 123 GGTGGACAGAACCTTAGACATCAAGTAATATTTTCTTAATTTGGCTATTCTGA 182
|||
Db 180 GCGGACTCGAGCTCCGCAACCCAGAACAACTTCTTCTGCTCAACCTGCGCATCTCGA 239
QY 183 CTTCCTCGTGGGTTTGATTTCCATCTCTGTATCCCTCACTGCTGTTG---TTTAAC 239
|||
Db 240 CTTCCTCGTGGGCTTCTGATCCACCTGATGTATGATCCCTAGCTGTGACAGCCGCTG 299
QY 240 GAATTTGGAGTGGAACTGCAATGTTTGTGCTCAATTAAGTATCTTTTGTGCAACGC 299
|||
Db 300 GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAGTGACCTACCTGTGCACTC 359
QY 300 ATCTGTCTCAATATTTGCTCATTAGCTAGGATCGATACAGTCACTTTCAAAATGCTGT 359
|||
Db 360 CTCTGCTTCAACATCTGCTCATACCTGCTAGCTAGACCGCTTCTGTGCTCACCGAGCGT 419
QY 360 GTCTTATAGGCTCAACACACTGCAATCAATGAAGATTGTTGCTCAAAATGCTGCTTTG 419
|||
Db 420 CTCAATCCGGGCCAGAGGCTGACACGCGGGGAGTGCGGAAGATGCTGTGCTGTTG 479
QY 420 GATCTAGGCTTCTTGTGTAATGCGCGATGATTTCTGGCTTTCAGAT-----TCTTGGAA 473
|||
Db 480 GGTGCTGGCTTCTGCTGTACGACACGAGCCATCTGAGCTGGGAGTACCTGTCGGGG 539
QY 474 GAACAGCAACACACAAAGACTGTGAGCTGGCTTGTGTTGACAGTGGTACATCTCAC 533
|||
Db 540 CAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTACAACTGGTACTTCTCAT 599
QY 534 CATTAATGCTCTTGGAACTCTGCTTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTG 593
|||
Db 600 CAGGCTTCCACCTGGAGTCTTACGCTTCTTACGCTTCTTACGCTTCTTAACTGACA 659
QY 594 GATTACTGAGCTGTGGAAGCTAGGCTCTCAG 629
|||
Db 660 CATCTACCTGAACATCCAGAGCGGACCGGCTCCG 695

RESULT 10

US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1

Query Match 11.9%; Score 140.4; DB 2; Length 2689;
Best Local Similarity 53.6%; Pred. No. 3.5e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

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QY 183 CTTCCTCGTGGGTTGATTTCCATTTCTGTATACATCCCTCAGCTGTTG---TTTAAC 239
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QY 240 GAATTTGGAGTGGAACTGCTGCTGTTTGGCTCATTAAGTATGCTCAATGCTGCTTTG 419
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QY 474 GAACAGCAACACAAAGACTGTGAGCTGCTGCTTTGTTTACAGAGTGTGATCTCTAC 533
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RESULT 11

US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/165,543

FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth A. Hanley
 REGISTRATION NUMBER: 33,505
 REFERENCE/DOCKET NUMBER: MNI-032CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2689 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 291..1625

US-09-165-543-1

Query Match 11.9%; Score 140.4; DB 3; Length 2689;
 Best Local Similarity 53.6%; Pred. No. 3.5e-34;
 Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCCGAGTCTACAGTAATGGCATCTTGCCACAGCTGTCTCAGGTCCTCGGCATTTT 62
 DB 350 GGCGCGCGCGGGCGCGCGCTTTCGCCAGCTGGAACCGGTGTCGCCGCT 409

QY 63 AATGCTCTCAATTGGCTTTGCTATAAATGATAGCAATGCTGTGTCATCTTAGCCTTTGT 122
 DB 410 CATGGCGTCTCATCGTGGCCACGGTGTGGGCAACGGCTGTGTCATGCTCGCTTCGT 469

QY 123 GGTGGACAGAACCCTAGACATCGAATTAATTTTTCTTAATTTGGCTATTCTGA 182
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QY 183 CTTCCTCGTGGGTTTGATTTCCATTCCTCTGATACATCCCTCACGTTG---TTTAACTG 239
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QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCATCTAGCTATCTTTCTGTGCAACGC 299
 DB 590 GACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTG 649

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 DB 710 CTCATACCGGCGCCAGCAGGCTGACACGCGCGGGCAGTGCAGGAGATGCTGCTGGTGTG 769

QY 420 GATAGTGGCTTTCTGTGTAATGGCCCGATGATCTTGGCTTTCAGAT-----TCTTGGAA 473
 DB 770 GGTGCTGGCCTTCTGTCTGTACGACCGACCATCTTCTGAGCTGGAGTACCTGTCCGGGG 829

QY 474 GAACAGCACGAACAAGAGCTGTGAGCTGGCTTTGTTACAGATGGTATCATCTCTAC 533

STREET: 830 CAGCTCCATCCCGGAGGCGCACTGCTATGCCGAGTTCTTTACAACTGGTACTCTCTCAT 883
 QY 534 CATTACAATGCTCTTTGGAAATTCCTCTTCTCTCATCTCTGTGGCTTATTTCAATGTACA 593
 DB 890 CACGGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGCGTCACCTCTTTTAACTCAG 949

QY 594 GATTTACTGGAGCCTGTGTGAAGCGTAGGGCTCTCAG 629
 DB 950 CATCTACCTGAACATCCAGAGCGCACCGGCTCG 985

RESULT 12
 US-09-167-354-5
 Sequence 5, Application US/09167354A
 Patent No. 6136559
 GENERAL INFORMATION:
 APPLICANT: Lovenberg, Timothy
 APPLICANT: Erlander, Mark
 APPLICANT: Pyati, Jayashree
 APPLICANT: Huvar, Arne
 TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
 FILE REFERENCE: JMW
 CURRENT APPLICATION NUMBER: US/09/167,354A
 CURRENT FILING DATE: 1998-10-07
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 5
 LENGTH: 2699
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: CDNA
 US-09-167-354-5

Query Match 11.9%; Score 140.4; DB 3; Length 2699;
 Best Local Similarity 53.6%; Pred. No. 3.5e-34;
 Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCCGAGTCTPAAACAGTAATGGCATCTTGCCACAGCTGTCTCAGGTCCTCGGCATTTT 62
 DB 358 GGCGCGCGCGGGCGCGCGCTTCTCGGAGCTGTGACCGCGGTGCTGGCCGCGCT 417

QY 63 AATGCTCTCAATTGGCTTTGCTATAAATGATAGCAATGCTGTGTCATCTTAGCCTTTGT 122
 DB 418 CATGGCGCTGCTCATCTGCGCCACGGTGTGGGCAACGGCTGTGTCATGCTCGCCTTGT 477

QY 123 GGTGGACAGAAAACCTTAGACATCGAAGTAATTTTTCTTAATTTGGCTATTCTGA 182
 DB 478 GGCCGACTCGAGCTCCGCCACCCAGAACAACTTCCTCTGCTCAACCTCGCCATCTCGA 537

QY 183 CTTCCTCGTGGGTTTGATTTCCATTCCTCTGATACATCCCTCACGTTG---TTTAACTG 239
 DB 538 CTTCCTCGTGGCGCTCTGTCATCCCACTGTATGATGACCTACGTGCTGACAGCGCGCTG 597

QY 240 GAATTTTGAAGTGAATCTGCAATCTGGCTCATTTTGGCTCATTTCTGACTATCTTTTGTGCAACGC 657
 DB 598 GACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTG 717

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QY 360 GTCTTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTG 419
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; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

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Best Local Similarity 53.6%; Pred. No. 3.5e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

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Db      358 GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGTGTGGCGCGCT 417
Qy      63 AATGCTCTTCATTTGCTTATAGTAAAGTAAATTTTCTTAATTTGGCTATTCTGA 122
Db      418 CATGGCGCTGCTCATGCTGGCCACGGTGTGGCAACGCGTGTGCTCGCTTCGT 477
Qy      123 GGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTCTGA 182
Db      478 GCGCGACTCGAGCTCCGACCCAGAACACTTCTTCTGCTCAACCTGCCATCTCCGA 537
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Qy      240 GAATTTTGGAGTGAATCTGCATGTTTGGCTCATCTACTGCTGCTGCTGACAGCGCGT 299
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; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORTI290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5
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Best Local Similarity 53.6%; Pred. No. 3.5e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy      3 GTCGGAGCTTAACAGTACTGCGATCTTGGCCACCAGCTGCTCAGTCCCTTGGCATTTT 62
Db      358 GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGTGTGGCGCGCT 417
Qy      63 AATGCTCTTCATTTGCTTATAGTAAAGTAAATTTTCTTAATTTGGCTATTCTGA 122
Db      418 CATGGCGCTGCTCATGCTGGCCACGGTGTGGCAACGCGTGTGCTCGCTTCGT 477
Qy      123 GGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTCTGA 182
Db      478 GCGCGACTCGAGCTCCGACCCAGAACACTTCTTCTGCTCAACCTGCCATCTCCGA 537
Qy      183 CTTCCTGCGGGTTGATTTCCATCTCTGTATACCTCCCTCAGCTGTG---TTTAACTG 239
Db      538 CTTCCTGCTGGCGCTTCTGCTATCCACTGTATGATGCTGCTGCTGCTGCTGCTGCTG 597
Qy      240 GAATTTTGGAGTGAATCTGCATGTTTGGCTCATCTACTGCTGCTGCTGCTGCTGCTG 299
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Qy      300 ATCTGCTACAAATATTTGCTCTCATTTAGCTACGATACGATACGATGCTGCTGCTGCT 359
Db      658 CTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTG 717
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	686.6	58.4	1173	13	US-09-875-076-13
5	686.6	58.4	1173	13	US-09-876-252-13
6	686.6	58.4	1173	14	US-10-052-193-1
7	686.6	58.4	1173	15	US-10-272-983-13
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15	686.6	58.4	1300	10	US-09-852-165-1	Sequence 1, Appli
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18	685	58.2	1173	15	US-10-290-078-26	Sequence 26, Appl
19	685	58.2	1265	15	US-10-290-078-25	Sequence 25, Appl
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22	172.8	14.7	2700	13	US-09-891-053-5	Sequence 5, Appli
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37	140.4	11.9	1335	17	US-10-727-021-6	Sequence 6, Appli
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42	140.4	11.9	2689	15	US-10-282-958-1	Sequence 1, Appli
43	140.4	11.9	2699	15	US-10-225-567A-548	Sequence 548, App
44	140.4	11.9	2699	17	US-10-727-021-5	Sequence 5, Appli
45	135.6	11.5	223	17	US-10-283-975A-697	Sequence 697, App

ALIGNMENTS

RESULT 1
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match 58.4%; Score 686.6; DB 9; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
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DB 1 ATGCCAGATACATAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCACTTT 60
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DB 61 TTTATGCTTTCATTTGCTTTGCTTATATGATGAGCAATGCTGTGGTCACTTTAGCCCTTT 120

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181 GACTTCTCTGGGTGATTTCCATTCCTCTGACATCCCTCAGCTGCTGTTTAACTGG 240
241 AATTTTGGAAAGTGAATCTGCATCTTTTGGCTCAATTAATCTGACTATCTTTTGTGACCGCA 300
241 GATTTTGGAAAGTGAATCTGCATCTTTTGGCTCAATTAATCTGACTATCTTTTGTGACCGCA 300
301 TCTGTCTACAATATGTCCTCATTAAGTACATGATCGATCCCTCAGCTGCTGTTTAACTGG 360
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361 TCTTATAGAACTCAACATCTGAGGCTCTTGAAGATTTGTTACTCTGATGGTGGCGTTTGG 420
361 TCTTATAGAACTCAACATCTGAGGCTCTTGAAGATTTGTTACTCTGATGGTGGCGTTTGG 420
421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATCTGTTGGAAGAACGC 480
421 GTGCTGGCTTTCTTAGTGAATGGCCGATGATTTCTAGTTTCAGAGTCTTTGGAAGAACGC 476
481 ACGAACAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATCTTCCGCAATCACA 534
541 ATGCTCTTGGATTCCTCTCTGATCTCTGCTGATCTCTGCTGCTTATTTCAATGTACAGATTTAC 600
535 TCATTCTTGGAAATTCGTGATCCGATCATCTTAGTCGCTTATTTCAATGAATTTAT 594
601 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGGCTCCCTAGCCATCTGCTGGAATTTCCACT 660
595 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGGCTCCCTAGCCATCTGCTGGAATTTCCACT 654
661 ACCTCTTCCAGTCTCAGGACATTTACAGAGCTGGGTGGCTTGGAGGAGTAAAT 720
655 GTCTCTTCCAACTCTGTGGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
721 CTTGATTTGAAGGAATCAGCTGCTCTGCTCACTCAGAAAGTCTTCGAAAGAAAGACGC 780
715 TCTGATCGACAGAGTTCCTGATCTCTTCAATTCAGAGACAGAGGAGAGTAGT 774
781 ATCTCTGGTCTCTTAAGGACTCACATGAACAGCAGTATCATCTGCCCTTCAAGTGGGTCC 840
775 CTCTGTTTCTCAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTCC 834
841 TTCTGGCGATCGGAAGTGCAGGCTTCGCAAGGAGTACGACAGCTTCTCAGAGGC 900
835 TTCTCCCAATCAGATCTCTAGTCTCTTCCAAAGGGAACATGTTGAACTGCTTAGAGCC 994
901 AGGAGCTAGCCAGGCTCACTGGCCATCTCTGAGGCTTTTGGCAATTTGCTGGGTCCA 960
895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTGTCTGTTGCTGGGTCCA 954
961 TACTGTCTGTTCACAAATGTCCTTCAACTTACCCAGGAACGGAACGCAATCGGTG 1020
955 TATTCTCTGTTCACAAATGTCCTTCAATTTAATCTCAGCAACAGGTCTTAATCAGTT 1014
1021 TGGTACAGATTCCTCTTGGCTGCAATGTTTCAATTCGTTTAACTCCCTTCTGTAC 1080
1015 TGGTATAGAAATTCATTTTGGCTTCTAGTGGTTCATTTCTTGTGCAATCTCTTTGTAT 1074
1081 CCTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGTACTTTGTGTGCAAAAGCAA 1140
1075 CCAATGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATATTTTGTATAAAAAGCAA 1134
1141 CCAAGCGCTGTACAGAAAC---CAGTCAAGTATCTTTTGA 1176
1135 CCTCTACCATCACAAACAGTGGTCTAGTATCTTTCTTAA 1173

RESULT 2
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Beigsmas, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match 58.4%; Score 686.6; DB 9; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGTCCCTTGGCATTT 60
DB 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGTCCCTTGGCATTT 60
QY 61 TTAATGCTCTCATTTGCTCTTAAATGAGTGAAGTCTGCTGCTATCTTAGCTTT 120
DB 61 TTAATGCTCTCATTTGCTCTTAAATGAGTGAAGTCTGCTGCTATCTTAGCTTT 120
QY 121 GTGGTGGACAGAACTTAGACATCGAAGTAAATATATTTTCTTAATTTGGCTATTCT 180
DB 121 GTGGTGGACAGAACTTAGACATCGAAGTAAATATATTTTCTTAATTTGGCTATTCT 180
QY 181 GACTTCTCTGGGTGATTTCCATTCCTCTGACATCCCTCAGCTGCTGTTTAACTGG 240
DB 181 GACTTCTCTGGGTGATTTCCATTCCTCTGACATCCCTCAGCTGCTGTTTAACTGG 240
QY 241 AATTTTGGAAAGTGAATCTGCATCTTTTGGCTCAATTAATCTGACTATCTTTTGTGACCGCA 300
DB 241 GATTTTGGAAAGTGAATCTGCATCTTTTGGCTCAATTAATCTGACTATCTTTTGTGACCGCA 300
QY 301 TCTGTCTACAATATGTCCTCATTAAGTACATGATCGATCCCTCAGCTGCTGTTTAACTGG 360
DB 301 TCTGTCTACAATATGTCCTCATTAAGTACATGATCGATCCCTCAGCTGCTGTTTAACTGG 360
QY 361 TCTTATAGAACTCAACATCTGAGGCTCTTGAAGATTTGTTACTCTGATGGTGGCGTTTGG 420
DB 361 TCTTATAGAACTCAACATCTGAGGCTCTTGAAGATTTGTTACTCTGATGGTGGCGTTTGG 420
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATCTGTTGGAAGAACGC 480
DB 421 GTGCTGGCTTTCTTAGTGAATGGCCGATGATTTCTAGTTTCAGAGTCTTTGGAAGAACGC 476
QY 481 ACGAACAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATCTTCCGCAATCACA 534
QY 541 ATGCTCTTGGATTCCTCTCTGATCTCTGCTGATCTCTGCTGCTTATTTCAATGTACAGATTTAC 600
DB 535 TCATTCTTGGAAATTCGTGATCCGATCATCTTAGTCGCTTATTTCAATGAATTTAT 594
QY 601 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGGCTCCCTAGCCATCTGCTGGAATTTCCACT 660
DB 595 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGGCTCCCTAGCCATCTGCTGGAATTTCCACT 654
QY 661 ACCTCTTCCAGTCTCAGGACATTTACAGAGCTGGGTGGCTTGGAGGAGTAAAT 720
DB 655 GTCTCTTCCAACTCTGTGGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CTTGATTTGAAGGAATCAGCTGCTCTGCTCACTCAGAAAGTCTTCGAAAGAAAGACGC 780
DB 715 TCTGATCGACAGAGTTCCTGATCTCTTCAATTCAGAGACAGAGGAGAGTAGT 774
QY 781 ATCTCTGGTCTCTTAAGGACTCACATGAACAGCAGTATCATCTGCCCTTCAAGTGGGTCC 840
DB 775 CTCTGTTTCTCAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTCC 834
QY 841 TTCTGGCGATCGGAAGTGCAGGCTTCGCAAGGAGTACGACAGCTTCTCAGAGGC 900
DB 835 TTCTCCCAATCAGATCTCTAGTCTCTTCCAAAGGGAACATGTTGAACTGCTTAGAGCC 994
QY 901 AGGAGCTAGCCAGGCTCACTGGCCATCTCTGAGGCTTTTGGCAATTTGCTGGGTCCA 960
DB 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTGTCTGTTGCTGGGTCCA 954
QY 961 TACTGTCTGTTCACAAATGTCCTTCAACTTACCCAGGAACGGAACGCAATCGGTG 1020
DB 955 TATTCTCTGTTCACAAATGTCCTTCAATTTAATCTCAGCAACAGGTCTTAATCAGTT 1014
QY 1021 TGGTACAGATTCCTCTTGGCTGCAATGTTTCAATTCGTTTAACTCCCTTCTGTAC 1080
DB 1015 TGGTATAGAAATTCATTTTGGCTTCTAGTGGTTCATTTCTTGTGCAATCTCTTTGTAT 1074
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGTACTTTGTGTGCAAAAGCAA 1140
DB 1075 CCAATGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATATTTTGTATAAAAAGCAA 1134
QY 1141 CCAAGCGCTGTACAGAAAC---CAGTCAAGTATCTTTTGA 1176
DB 1135 CCTCTACCATCACAAACAGTGGTCTAGTATCTTTCTTAA 1173

Db 955 TATTCTCTGTTCAAAATGTCCTTTCAATTTATTCTCCAGCAACAGGTCCTAAATCAGTT 1014

QY 1021 TGGTACAGATGCTCTGCTGCAATGGTTCATTCGTTGTTAAATCCCTTTCTGTAC 1080

Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTCCTTTGTCATTCCTTTTGTAT 1074

QY 1081 CCTTTGTTGTCAGGCGTTTCCAGAGGCTTTCTGGAAGATCTTTGTTGTCACAAAGCAA 1140

Db 1075 CCAATGTTGTCACAGCGCTTTCAAAGGCTTTCTTGAAAAATTTTGTATATAAAGCAA 1134

QY 1141 CCAGCGCTGTCCAGAAC--CAGTCAGTATCTTCTGA 1176

Db 1135 CCTTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 5

US-09-876-252-13

Sequence 13, Application US/09876252

Publication No. US20030018182A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Lehmann-Bruinsma, Karin

APPLICANT: Chalmers, Derek T.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Lin, I-Lin

APPLICANT: Dang, Huong T.

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor

FILE REFERENCE: AREN-0054

CURRENT APPLICATION NUMBER: US/09/876,252

CURRENT FILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: 09/416,760

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/110,060

PRIOR FILING DATE: 1998-11-27

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,852

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/109,213

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/123,944

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,945

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,948

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,951

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/152,524

PRIOR FILING DATE: 1999-09-03

PRIOR APPLICATION NUMBER: 60/151,114

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: 60/108,029

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,439

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,127

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,131

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/141,448

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/156,555

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,634

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,653

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/157,280

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,294

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,281

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,282

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/156,633

NUMBER OF SEQ ID NOS: 146

SOFTWARE: Patentin version 3.0

SEQ ID NO 13

LENGTH: 1173

TYPE: DNA

ORGANISM: Homo sapiens

US-09-876-252-13

Query Match 58.4%; Score 686.6; DB 13; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2e-209;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAAACAGTACTGGCATCTTGCACACAGTGTCTCAGTCCCTTTGGCATTT 60

Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCATAAGCACTCGTGTACTTAGCATTT 60

QY 61 TTAATGCTCTTCAATTTGCGCTTTGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCCTTT 120

Db 61 TTTATGCTCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCCTTT 120

QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAAATTTATTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCCATCTCT 180

QY 181 GACTTCTCTGGGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTTAACTGG 240

Db 181 GACTTCTTTGGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGCTGTGTTTAACTGG 240

QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGGCACCGCA 300

Db 241 GATTTTGGAAAGAAATCTGTGTAATTTTGGCTCCTACTGACTATCTTTTATGTACAGCA 300

QY 301 TCTGTCTACAATPATTTGCTCCTCAATAGCTACGATCCGATCCAGTCCAGTTCCTCAATGCTGG 360

Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCCATACCTGTGCTCAGTCTCAATGCTGG 360

QY 361 TCTTATAGGCTCAACACACTGGCATCATGAGATTTGTTGCTCAAAATGCTGGCTGTTGG 420

Db 361 TCTTATAGAACTCAACATACTGGGCTCTTGAAGATTTGTTACTCTCATGCTGGTGGCTTTGG 420

QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATCTGGCTTCAGATCTTGGAAAGACAGC 480

Db 421 GTGCTGGCTTTCTTAGTGAATGGGCCAATGANTTTAGTTTTCAGAGTCTTTGGAAGGA--- 476

QY 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGTGATCATCTCCATCCATTCACA 540

Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAAATGGTATCATCTTGGCCATCACA 534

QY 541 ATGCTTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600

Db 535 TCATTTCTTGAATTCGTGATCCAGTCCATCTTAGTGGCTTATTTCAACATGAATTTAT 594

QY 601 TGGAGCTGTGGAAGCGTAGGCTCTCAGTAGGTGGCTTAGCCATGCTGGATTTCTCACT 660

Db	595	TGAGCGCTGTGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCGACTGACTGCT	654	Db	121	GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTTTTCTTAACCTGGCCATCTCT	180
Qy	661	ACCTCTTCAGAGTCTTCAGGACACTTACACAGAGCTGGGTGGCTTCAGGACCAAGTAAT	720	Qy	181	GACTCTCTCGTGGGTTTGATTTCCATTCCTCTGTA CANCTCTCAGCTGGTGTGTTTAACGG	240
Db	655	GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714	Db	181	GACTCTTGTGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTCTTCGAATGG	240
Qy	721	CTTGATTAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGCAGC	780	Qy	241	AATTTTGAAGTGGAACTCTGCATGTTTGGCTCAATTAAGTCTGCTTCTTTGTGCAACGCA	300
Db	715	CTGCAATCGAAGATTCCTGCACTCTTTTCAATTCAGAGACAGAGAGAAAGTAGT	774	Db	241	GAITTTGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTTGTGTACAGCA	300
Qy	781	ATCTGTGTCTTAAAGACTCACATGAACAGCACTATCTGCTTCAAAGTGGGTTC	840	Qy	301	TCGTCTTACAAATATGTCCTCATTTAGTACGATCGATACCAAGTCAAGTCAAAATGCTGTG	360
Db	775	CTCAATTTTCTCAAGAACCAAGATGATAGCAATGATTTTCTTCCAAAATGGGTTC	834	Db	301	TCGTATATTAACATTTGCTTCACTAGCTATGATCGATACCTGTGCTCAATGCTGTG	360
Qy	841	TTCTGGCATGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGCAGAGCTTCTCAGAGCG	900	Qy	361	TCATTATAGGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGCTGCTGTTGG	420
Db	835	TTCTCCCAATCAGATTCGTAGCTCTTCAACCAAGGGAACATGTTGAACCTGCTTAGAGCC	894	Db	361	TCATTATAGAACTCAACATACTGGGCTCTGAAGATTTGTTACTCTGATGGTGGCGTTGG	420
Qy	901	AGGAAGTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCCATTTTGGCTGGCTCCA	960	Qy	421	ATATCGGCTTCTTGGTAAATGGCCGATGATTCGGCTTCAGATTCCTTGAAGAAACAGC	480
Db	895	AGGAGATTAGCCAAAGTCACTGGCCATCTTCTTAGGGGTTTTTGGCTGGCTGGCTCCA	954	Db	421	GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTAGTTTCAGAGTCTTGGAAAGAA	476
Qy	961	TACTGTCTGTTCACAATTTGCTTCAACTTACCCAGAACGGAAGCCCAAAATCGGTG	1020	Qy	477	--TGAAAGGTAGTAATGTAACCTGGATTTTTCGGAATGATGATCTTGGCCATCACA	534
Db	955	TATTCCTCTTCACAATTTGCTTCACTTCAACCAAGGGAACATGTTGAACCTGCTTAGAGCC	894	Db	541	ATGCTCTTGAATTTCTGCTTCTGCTCACTCTGCTGCTGCTTCAATGATGATGATTTAC	600
Qy	1021	TGTTACAGCATTTGCTTCTGCTGCAATGTTCAATTCGTTTGTGTTTAAATCCCTTCTGTAC	1080	Qy	541	ATGCTCTTGAATTTCTGCTTCTGCTCACTCTGCTGCTGCTTCAATGATGATGATTTAC	600
Db	1015	TGTTATAGAAATTCATTTTGGCTTCAGTGGTCAATTCCTTGTCAATCTCTTGTAT	1074	Db	535	TCATTCTTGAATTCGTTGATCCAGTCCATCTAGTCTGCTTATTTTCAACATGAATATTTAT	594
Qy	1081	CTTTTGTGTACAGGGGTTTTCCAGAAAGGCTTCTGGAAGATCTTTGTGTGCAAAAGCAA	1140	Qy	601	TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCTCCACT	660
Db	1075	CCATTGTGTACAAAGCGCTTTCAAAAGGCTTTCCTTGAAGAAATTTTGTATTAAGGCAA	1134	Db	595	TGGAGCTGTGGAAGCGTAGGATCATCTCAGTAGGTGCCAAAGCCATCTTGGACTGCTGCT	654
Qy	1141	CGAGCGGTGTACAGAAC---CAGTCAGTATCTTCTTGA	1176	Qy	661	ACCTCTTCCAGTGTTCAGGACACTTACACAGAGCTGGGCTGCTTGCAGGACCAAGTAAT	720
Db	1135	CCTCTACCATCAACAACAGCTCGGTGAGTATCTTCTTAA	1173	Db	655	GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
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US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1
Query Match 58.4%; Score 686.6; DB 14; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAAGCTGCTCAGGTCCCTTGGCATTT 60
Db 1 ATGCCAGATCTAATAGCAAAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 61 TTAATGCTTCATTTGCTTTGCTTAAATGCTAGGCAATGCTGGTCACTCTTAGCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTTTCTTAAATTTGGCTATTTCT 180

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; Sequence 13, Application US/10272993
; Publication No. US20030148450A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
;
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
;

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Query Match 58.4%; Score 686.6; DB 15; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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RESULT 8
US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Heate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: FC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-354-769-1

Query Match 58.4%; Score 686.6; DB 15; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2e-209; Mismatches 284; Indels 9; Gaps 2;

Matches 886; Conservative 0;

QY 1 ATGTCGGAGTCTAAACAGTACTGGCACTTTGGCCAGCTGCTCAGGTCCTCCCTTGCAATTT 60

Db 1 ATGCCAGATCAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

QY 61 TTAATGCTTCATTTGCCCTTTGCTATATAAATGGTAGCAATGCTGTGGTCACTTTAGCCCTTT 120

Db 61 TTTATGTCCTTAGTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120

QY 121 GTGCTGGACAGAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTAATTTCT 180

Db 121 GTGCTGGACAGAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTAATTTCT 180

QY 181 GACTTCTCTCGGGGTTTGATTTCCATTCCTCTGTACATCCCTCACTGCTGTGTTAACTGG 240

Db 181 GACTTCTCTCGGGGTTTGATTTCCATTCCTCTGTACATCCCTCACTGCTGTGTTAACTGG 240

QY 241 AATTTTGAAGTGAATCTGCAATGCTTTTGGCTCACTACTGACTATCTTTGTGCAACGCA 300

Db 241 GATTTTGAAGTGAATCTGCTATTTTGGCTCACTACTGACTATCTTTGTGCAACGCA 300

QY 301 TCTGCTACAAATTTGCTCTAATAGCTAGCATGATGATGCTGCTGCTGCTGCTGCTGCTG 360

Db 301 TCTGCTACAAATTTGCTCTAATAGCTAGCATGATGATGCTGCTGCTGCTGCTGCTGCTG 360

QY 361 TCTGCTATGAACTCAACATGCTGGGCTTTGAAAGATGTTTACTCTGATGCTGGCCGCTTGG 420

Db 361 TCTGCTATGAACTCAACATGCTGGGCTTTGAAAGATGTTTACTCTGATGCTGGCCGCTTGG 420

QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTGGCTTCAATGCTGCTGCTGCTGCTGCTG 480

Db 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTGGCTTCAATGCTGCTGCTGCTGCTGCTG 480

QY 481 ACGAACACAAAGACTGTGAGCTGCTGCTTTGTTACAGAGTGTATCACTCTCAACATACA 540

Db 481 ACGAACACAAAGACTGTGAGCTGCTGCTTTGTTACAGAGTGTATCACTCTCAACATACA 540

QY 477 --TGAAGTGTGAATGTGAACCTGGATTTTTCGAAATGTTATCTTCCAGAGTCTTTGGAAGGA --- 476

Db 477 --TGAAGTGTGAATGTGAACCTGGATTTTTCGAAATGTTATCTTCCAGAGTCTTTGGAAGGA --- 476

QY 541 ATGCTCTTTGGAATTCCTGCTCTCTGCTCATCTCTGCTGCTTATTTCAATGATACAGATTTAC 600

Db 541 ATGCTCTTTGGAATTCCTGCTCTCTGCTCATCTCTGCTGCTTATTTCAATGATACAGATTTAC 600

QY 535 TCATTTCTTGAATTCCTGATCCAGTCACTCTTAGTCCGCTTATTTCAACATGAATATTTAT 594

Db 535 TCATTTCTTGAATTCCTGATCCAGTCACTCTTAGTCCGCTTATTTCAACATGAATATTTAT 594

QY 601 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGCTGCTGCTGCTGCTGCT 660

Db 601 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGCTGCTGCTGCTGCTGCT 660

QY 595 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGCTGCTGCTGCTGCTGCT 654

Db 595 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGCTGCTGCTGCTGCTGCT 654

QY 661 AACTCTTCAGTCTTTCAGACACTTACACAGAGCTGGGCTGGCTTGCAGGACCAAGTAAT 720

Db 661 AACTCTTCAGTCTTTCAGACACTTACACAGAGCTGGGCTGGCTTGCAGGACCAAGTAAT 720

QY 655 GTCTCTTCCAACTCTGTGGACACTCTTTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

Db 655 GTCTCTTCCAACTCTGTGGACACTCTTTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 721 CTTGGAATGAAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

Db 721 CTTGGAATGAAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 715 TCTGCTATCAGCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774

Db 715 TCTGCTATCAGCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774

QY 781 ATCTGGTGTCTTAAAGTGTACATGAAACAGAGTATCACTGCTTCAAGTGGGTTC 840

Db 781 ATCTGGTGTCTTAAAGTGTACATGAAACAGAGTATCACTGCTTCAAGTGGGTTC 840

QY 775 CTCATGTTTCTTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834

Db 775 CTCATGTTTCTTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834

QY 841 TCTGCGATCGGAAAGTGCAGGCTTTCGCAAGAGGAGTACGACAGCTTCTCAGAGGC 900

Db 841 TCTGCGATCGGAAAGTGCAGGCTTTCGCAAGAGGAGTACGACAGCTTCTCAGAGGC 900

QY 835 TTCTCCCAATCAGATCTGTAGCTCTTCAACCAAGGGAACATGTTGAATGCTTTAGAGCC 894

Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCAACCAAGGGAACATGTTGAATGCTTTAGAGCC 894

QY 901 AGGAAGCTACCCAGGTCAGTGGCCATCTCTCTGAGCGCTTTTGGCAATTTGCTGGCTCCA 960

Db 901 AGGAAGCTACCCAGGTCAGTGGCCATCTCTCTGAGCGCTTTTGGCAATTTGCTGGCTCCA 960

Db 895 AGGAGATTAGCCAAAGTCACTGGCCCATCTCTTAGGGGTTTTTGTGCTGTTGCTGGCTCCA 954

QY 961 TACTGTCTGTTCACAATTTGCTCTTTCAACTTACCCAGAACGCGCCCAAAATCGGTG 1020

Db 955 TATTCTGTTCACAATTTGCTCTTTCAACTTATTTCCCTCAGCAACAGGTCCTAAATCAGTT 1014

QY 1021 TGGTACAGCATTTGCTCTTCTGCTGCAATGTTCAATTCGTTTGTATATCCCTTTCTGTAC 1080

Db 1015 TGGTATAGCAATTTGCTCTTCTGCTGCAATTTCAATTCGTTTGTATATCCCTTTCTGTAC 1074

QY 1081 CTTTGTGTACAGGCGTTTCCAGAGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140

Db 1075 CCAATGTGTACAGGCGTTTCCAGAGCTTTCTGGAAGATACCTTTGTGTGATATAAAGCAA 1134

QY 1141 CCAGCGTGTACAGAAAC--CAGTCAGTATCTTCTTGA 1176

Db 1135 CCTTACCATCACACACAGTCGTCAGTATCTTCTTAA 1173

RESULT 9

US-10-393-807-13

; Sequence 13, Application US/10393807

; Publication No. US20030175891A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

; FILE REFERENCE: AREN0050

; CURRENT APPLICATION NUMBER: US/10/393,807

; CURRENT FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: US/09/417,044

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,851

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,949

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/136,436

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,437

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,567

; PRIOR FILING DATE: 1999-05-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-393-807-13

Query Match 58.4%; Score 686.6; DB 15; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2e-209;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAAACAGTACTGGCACTTTGGCCAGCTGCTCAGGTCCTCCCTTGCAATTT 60

Db 1 ATGCCAGATCAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

QY 61 TTAATGCTTCATTTGCCCTTTGCTATATAAATGGTAGCAATGCTGTGGTCAATCTTAGCCTTT 120

Db 61 TTTATGCTCTTAGTAGCTTTTGCTATATAATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120

121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT 180
121 GTGGTGACAAACCTTAGACATCGAAGTAGTATATTTTCTTAATTTGGCCATCTCT 180
181 GACTTCTCGTGGTGTGATTTCAATTCCTCTGTACATCCCTACGCTGTGTTTAACTGG 240
181 GACTTCTTGTGGGTGTGATCTCCATTCCTTGTGTACATCCCTACACGCTGTTCGAATGG 240
241 AATTTTGGAGTGGAACTCTGATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
241 GATTTTGGAAAGAAATCTGTGTAATTTGGCTCTACTGACTATCTGTTATGTACAGCA 300
301 TCTGTCTPACAATATGTCTCATTAGCTACGATCAGATACCAGTCAGTTCCTCAAAATGCTGTG 360
301 TCTGTATATAACATTTGCTCATCAGCTATGATGATACCTGTGTCAGTCTCAATGCTGTG 360
361 TCTTATAGGCTCAACACATCGCATCATGAAGATTTGTTGCTCAAAATGCTGTGTTGG 420
361 TCTTATAGAACTCAACATCTAGGCTCTTGAAGATTTGTTACTCTGTGATGCTGGCGTTGG 420
421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGCTTTCAGATTTCTGGAAGAACAGC 480
421 GTGCTGGCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA---- 476
481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTTACAGAGTGGTACATCTCCATCACCATPACA 540
477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCACA 534
541 ATGCTCTTGAATTCCTGCTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTTAC 600
535 TCATTTCTGGAATTCGTGTATCCAGTCACTCTTAGTCTGCTTATTTCAACATGAATATTTAT 594
601 TGGAGCTGTGGAAGGTAGGGCTCTCAGTAGTGGCCTAGCCATGCTGGAATCTCCACT 660
595 TGGAGCTGTGGAAGGTAGTATCTCAGTAGTGGCCAAAGCCATCTCGACTGACTGCT 654
661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGTGGGGTGGCTTTCAGGACAAAGTAAT 720
655 GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
721 CCTGGAATAGGAATCAGCTGATCTGTCATCTCAGAAAGTCTCTCAGAAAGAGAGC 780
715 TCTGCAATCAGACAAAGTTCCTGCTATCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
781 ATCTCTGTGCTTAAAGGACTCATGACGACAGAGATATCACTGCTTCAAGTGGGTTCC 840
775 CTCATGTTTTCTTCAAGAACCAAGATGATAGCAATACAAATGCTTCCAAATGGGTTCC 834
841 TTCTGGCGATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGAGTCTTCTCAGAGGC 900
835 TTCTCCCAATCAGATTTCTGTAGCTCTTCAACAAAGGGAACATGTTGAATGCTTAGAGCC 894
901 AGGAAGCTAGCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960
895 AGGAGATAGCAGAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTTGCTGGGCTCCA 954
961 TACTGTCTGTTTCACAATTTGCTTTTCAACTTACCAGAACGGAAGCCCAATCGGTG 1020
955 TATTCTCTGTTTCACAATTTGCTTTCAATTTATTCCTCAGAACAGGTCTTAAATCAGTT 1014
1021 TGGTACAGATTCGCTTCTGGCTGCAATGGTTCGAATGCTTGTGTTTAAATCCCTTTCTGTAC 1080
1015 TGGTATAGAATTCATTTTGGCTTCAAGTGTTCATTTCTTGTGATTCCTCTTTTGTAT 1074
1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTTGGAAAGATCTTTGTGTGACAAAGCAA 1140
1075 CCATTTGTGTACAGGCGCTTTCAAAAGGCTTCTTGAATAATTTTGTATATAAAAGCAA 1134
1141 CCAGCGCTGTCAAGAAC---CAGTCAGTATCTTTTGA 1176
1135 CCTTACCATCAACACAGTCTGGTCAGTATCTTCTTAA 1173

RESULT 10

US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7 US28 CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2

SEQ ID NO 13

LENGTH: 1173

TYPE: DNA

ORGANISM: Homo sapiens

US-10-417-820A-13

Query Match 58.4%; Score 686.6; DB 16; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2e-209;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAAACAGTACTGGCATCTTGGCCACCGAGCTGCTCAGGTCCCTTGGCATTTT 60

Db 1 ATGCCAGATCTATATAGCACAATCAATTTATCTACTAAGCACCTCGTGTACTTTAGCATTT 60

QY 61 TTAAGTCTTCAATTTGGCTTTGCTATAATGTTAGGCAATGCTGTGGTCATCTTAGCCTTT 120

Db 61 TTATGCTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGCTCATTTTAGCTTTT 120

QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATTTGGCCATCTCT 180

QY 181 GACTTCTCGTGGTGTGATTTCCATTCTCTGTACATCCCTCAGCTGTGTTTAACTCG 240

Db 181 GACTTCTTGTGGGTGTGATCTCCATTCTTTGTACATCCCTCAGCTGTGTTTAACTCG 240

QY 241 AATTTTGGAAAGTGAATCTGTCATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300

Db 241 GATTTTGGAAAGAAATCTGTGTAATTTGGCTCAGTACTGACTATCTGTTATGTACAGCA 300

QY 301 TCTGTCTCAATATTTGCTCTCTATTAGCTACGATCGATACAGTCTGTTTCAAAATGCTGTG 360

Db 301 TCTGTATATAACATTTGCTCTCATGATGATGATGATGATGATGATGATGATGATGATG 360

QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420

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Db 361 TCCTATAGACTCAACATCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
Qy 421 ATATCGGCTTTCTTGGTAATATGGCCGAGATCTTGGCTTCAGATTCCTGGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTAGTGAATGGGCAATGATCTTAGTTTCAGAGTCTTGGGAAGCA---- 476
Qy 481 ACAGAACAAAGGACTGTGAGCGTGGCTTCTTACAGAGTGATGATCTCCTCACCATTACA 540
Db 477 --TGAAGGTAGTGAATGGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 535 TCATTTCTTGGAAATCTGTCATCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 594
Qy 601 TGGAGCTGTGGAGCGTAGGGCTCTCAGTAGTGCCCTAGGCTGCTGGATCTCCACT 660
Db 595 TGGAGCTGTGGAGCGTAGGATCTCTCAGTAGTGCCCAAGCCATCTCTGGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTCTTCCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAGTAAT 720
Db 655 GTCTCTTCCACATCTGTGGACATCTATCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CTTGATTTGAAGGATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 715 TCTGATCTGACAGAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 774
Qy 781 ATCTGGTGTCTTGAAGACTCAGATGAACAGCAGTATCAGTCCCTTCAAGTGGTTC 840
Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834
Qy 841 TTCTGGGATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTGCAGAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGTCTTCCACCAAGGGACATGTTGAAGTCTGTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGCTCAGTCCCATCTCTCTGAGCGCTTTTGGCCATTTGCTGGGCTCA 960
Db 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTGCTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTACAAATTTGCTTTCACTTACCCAGAGCGGAGCCCAAAATCGGTG 1020
Db 955 TATTCTGTGTTCACAATTTGCTTTCACTTTATCTCTCAGCAACAGGCTCTAAATCAGTT 1014
Qy 1021 TGCTACAGATTCCTCTCTGCTGCAATGGTTCAATTCGTTGTTAACTCCCTTCTGTAC 1080
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Db 1075 CCATTTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATAAAAAAGCAA 1134
Qy 1141 CCAGCGCTGTCCAGAAC---CAGTCAGTCTCTCTTGA 1176
Db 1135 CCTTACCATCAACAACAGTGGGTGAGTATCTTCTTAA 1173
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RESULT 11
US-10-723-955-13
; Sequence 13, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
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; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-955-13

Query Match 58.4%; Score 686.6; DB 17; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGGATCTTGGCCACAGCTGCTCAGTCCCTTGGCATTT 60
Db 1 ATGCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 61 TTAATGCTTCAATTTGCTTCTTCTATATGTTAGGCAATGCTGCTGATCTTACCTTTT 120
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Db 301 TCTGTATATACATTTGCTCTCATCAGCTATGATCGATACCTGCTCAGTCTCAAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGGATCATGAAGATGTTTGTCTCAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACATCTGGGCTTTGAAGATTTGTACTCTGATGGTGGCCGTTGG 420
Qy 421 ATACTGGCTTCTTCTGTAATGGCCGATGTTTCTGGCTTCAAGTCTCAGATTTCTTGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTCTGTAATGGCCGATGTTTCTGATTTTCAAGTCTTGGAGGA---- 476
Qy 481 ACAGAACAAAGGACTGTGAGCTTGGCTTTGTTTACAGAGTGTGATCTCTCACCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATGTTTCTGATGGTGGCTTT 534
Qy 541 ATGCTCTTGGAAATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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Db 535 TCATCTTGGAAATTCGTCATCCAGTCATCTAGTCGCTATTATTCACATGAATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTCAGCAATGCTGGATTCCTCACT 660
Db 595 TGGAGCCTGTGGAAGCGTAGATCATCTCAGTAGGTGCCAAAGCCATCTGGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTCGAGCACAAGTAAT 720
Db 655 GTCTCTTCCAAACATCTGTGGACATCATTCAGAGGTAGACTATCTTCAGAGGATCTCTT 714
Qy 721 CTTGGATTGAAGGAATCAGTGTGATCTCTGTCACCTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Db 715 TCTGATCGACAGAAGTTCCTGTCATCTTCAATTCAGAGACACAGAGGAGAGAGTAGT 774
Qy 781 ATCTGTGTGCTTAAAGACTCATGAAACAGAGTAGTATCATCTGCTTCAAGTGGGTTC 840
Db 775 CTCATGTCTTCCCAAGAACCAAGATGAATAGCAATACAATTCCTTCCAAATGGGTTC 834
Qy 841 TTCTGGGATCGGAAGTGCAGGCTTCGCCAAAGGGAGTAGCAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCCTGTCATCTTCAATTCAGAGACACAGAGGAGAGAGTAGT 894
Qy 901 AGAAGCTAGCAGGTCAGTGGCCATCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGGCTGCCA 954
Qy 961 TACTGTCTGTTCACAAATGTCTTCACTTACCTTACCTTACCTTACCTTACCTTACCTT 1020
Db 955 TAITCTCTGTTCACAAATGTCTTCACTTACCTTACCTTACCTTACCTTACCTTACCTT 1014
Qy 1021 TGGTACAGCAATTCGCTTCTGCTGCAATTCGATTCGATTCGATTCGATTCGATTCGATTC 1080
Db 1015 TGGTATAGAAATTCGATTCGCTTCACTTACCTTACCTTACCTTACCTTACCTTACCTT 1074
Qy 1081 CTTTGTGTTCACAGGCTTTCAGAAAGCTTTCGGAAGATPACTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAAAGCTTTCAAAGGCTTTCGGAAGATPACTTTGTGTGACAAAGCAA 1134
Qy 1141 CCAGGCTGTTCACAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACAAACAGTCGTCGTCAGTATCTTCTTAA 1173

RESULT 12
US-10-737-619-1
; Sequence 1, Application US/10737619
; Publication No. US20040138234A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PCL0963A
; CURRENT APPLICATION NUMBER: US/10737,619
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-619-1

Query Match 58.4%; Score 686.6; DB 17; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGAGTCTAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 ATGCCAGATCTAATAGCACAATCAATTTATCCTAAGCACTCGTGTACTTTAGCAATTT 60
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Qy 481 ACGAACACAAGGACTGTGAGCTGGCTTTGTTTACAGAGTGGTACATCTCTCACCATPACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTGCCATCACA 534
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Db 535 TCATCTTGGAAATTCGTGATCCCACTCATCTTAGTGGCTTATTTTCAACATGAATATTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCCTCACT 660
Db 595 TGGAGCCTGTGGAAGCGTAGATCATCTCAGTAGGTGCCAAAGCCATCTGAGCTACTGCT 654
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Db 655 GTCTCTTCCAAACATCTGTGGACACTATTTCAGAGGTAGACTATCTTCAAGAGAGATCTCT 714
Qy 721 CCTGGATTGAAGNAATCAGTGTGCTCTCAGTACCTCAGAAAGTCTCTGAAAGAGAGCAGC 780
Db 715 TCTGATCGACAGAAGTTCCTGTCATCTCTTCAATTCAGAGACACAGAGGAGAGAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGGACTCATGAACAGCAGATATCACTGCTTCAAAGTGGGTTC 840
Db 775 CTCATGTTTCTCAGAACCAAGATGAATAGCAATTAATTTGCTTCCAAATGGGTTC 834
Qy 841 TCTGGGATCGGAAGTGCAGGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900
Db 835 TCTTCCCAATCAGATTCCTGTCATCTTCAACAAAGGGAACATGTTGAATCTTAGAGCC 894
Qy 901 AGAAGCTAGCAGGTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 960
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Qy 961 TACTGTCTGTTCACAAATGTCTTCACTTACCTCAGAAAGCGGAACGCCCAATTCGGT 1020
Db 955 TATCTCTGTTCACAAATGTCTTCAATTTATCTCAGCAACAGCTCTTAATTCAGTT 1014
Qy 1021 TGGTACAGCAATTCGCTTCTGCTGCAATGCTTCAATTCGTTTGTATTCCTTCTGTATC 1080
Db 1015 TGGTATAGAAATTCGATTTTGGCTTTCAGTGGTTCAAATTCCTTTGTCAATCTCTTTGTAT 1074
Qy 1081 CTTTGTGTTCAGAGGCTTTCAGAGAGCTTCTGGAAGTACTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTTCAGAGGCTTTCAAAGGCTTCTTGAAGATATTTTGTATATAAAGCAA 1134
Qy 1141 CCAGGCTGTTCACAGAAC---CAGTCAGTATCTTCTTGA 1176
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Ds	1135	CCTTACCATCACAACAGTCGGTCAGTATCTTTCTTAA	1173
RESULT 13			
US-10-782-596-13			
; Sequence 13, Application US/10782596			
; Publication No. US20040137509A1			
; GENERAL INFORMATION:			
; APPLICANT: Chen, Ruoping			
; APPLICANT: Dang, Huong T.			
; APPLICANT: Liaw, Chen W.			
; APPLICANT: Lip, I-Lin			
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors			
; FILE REFERENCE: AREN0050			
; CURRENT APPLICATION NUMBER: US/10782,596			
; CURRENT FILING DATE: 2004-02-19			
; PRIOR APPLICATION NUMBER: US/09/875,076			
; PRIOR FILING DATE: 2001-06-06			
; PRIOR APPLICATION NUMBER: 09/417,044			
; PRIOR FILING DATE: 1999-10-12			
; PRIOR APPLICATION NUMBER: 60/120,416			
; PRIOR FILING DATE: 1999-02-16			
; PRIOR APPLICATION NUMBER: 60/121,851			
; PRIOR FILING DATE: 1999-02-26			
; PRIOR APPLICATION NUMBER: 60/123,946			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/123,949			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/136,436			
; PRIOR FILING DATE: 1999-05-28			
; PRIOR APPLICATION NUMBER: 60/136,437			
; PRIOR FILING DATE: 1999-05-28			
; PRIOR APPLICATION NUMBER: 60/136,439			
; PRIOR FILING DATE: 1999-05-28			
; PRIOR APPLICATION NUMBER: 60/136,567			
; PRIOR FILING DATE: 1999-05-28			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 13			
; LENGTH: 1173			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-782-596-13			
Query Match 58.4%; Score 686.6; DB 17; Length 1173;			
Best Local Similarity 75.1%; Pred. No. 2e-209;			
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;			
Qy	1	ATGTCGGAGCTTAACAGTACTCGGCATCTTGCCACAGCTGTCTAGGTCCTCCCTTGGCAATT	60
Ds	1	ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTGTACTTTAGCAATT	60
Qy	61	TAAATGCTTCAATTTGGCTTTGCTATATGTAGGCAATGCTGGTCACTCTTAGCCTTT	120
Ds	61	TTTATGCTCTTAGTAGCTTTTGGCTATATGTAGGAATGCTTTGGTCAATTTAGCTTTT	120
Qy	121	GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAAATTTGGCTATTTCT	180
Ds	121	GTGGTGGACAAAACCCTTAGACATCGAAGTAGTATTTTTTCTTAACTTGGCCATCTCT	180
Qy	181	GACTTCCTCGTGGGTTTGATTTCCAATTCCTCTGTAFACATCCCTCAGCTGTGTTTAATG	240
Ds	181	GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCAGCTGTGTTGAATGG	240
Qy	241	AATTTTGAAGTGAATCTGCAGTTTTGGCTCACTACTGACTATCTTTTGTGACACGCA	300
Ds	241	GATTTTGAAGAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA	300
Qy	301	TCTGTCTCAATATTTGCTTCAATAGTACGATGATACCAAGTCAAGTTTCAAATGCTGTG	360
Ds	301	TCTGTATATAACATTTGCTTCAATCAGCTATGATGATACCTGTCAGTCTCAAATGCTGTG	360

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1197)
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-5

Query Match 58.4%; Score 686.6; DB 10; Length 1266;
Best Local Similarity 75.1%; Pred. No. 2.1e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGCTAAACAGTACTGGCATCTTGCACAGCTGTCAGGTCCCTTGGCATTT 60
DB 25 ATGCCAGATACCTAATAGCACAACTCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 84

QY 61 TTAATGTCTTCATTTGGCTTTGCTATAATGGTAGCAATGCTGTGTCATCTTACGCCCTTT 120
DB 85 TTTATGCTCTTAGTAGCTTTTGTATATAGCTAGGAATGCTTGGTCAATTTTACCTTTT 144

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DB 145 GTGGTGACAGAACTTTAGACATCGAAGTAGTTAATTTTTCTTAATTTGGCTATTTCT 204

QY 181 GACTTCCTCGGGTTTGAATTTCAATCTCTGTACATCCCTCAGGTGTTGTTAACTGG 240
DB 205 GACTTCCTCGGGTTGATCTCCATCTCTTTGTACATCCCTCAGGTGTTGTTAACTGG 264

QY 241 AATTTTGGAACTGGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300
DB 265 GATTTTGGAAAGAACTGTTGTTTGGCTCACTGACTATCTGTTAATGACAGCA 324

QY 301 TCTGTACAAATATGCTCTCATTAGCTACGATACGATACAGTACAGTTTCAAACTGCTGT 360
DB 325 TCTGTATATAACATTTCTCATCAGCTATGATGATACCTGTGAGTCTCAAACTGCTGT 384

QY 361 TCTATAGGCTCACAACATGCGATCATGAAGATTGTTGCTCAAACTGCTGCTTTGG 420
DB 385 TCTATAGAACTCAACATGCTGAGGCTCTGAAGATTGTTACTGATGTTGGCGCTTTGG 444

QY 421 ATACTGCTTTCTTGGTAAATGGCCGATGATTTCTGCTTCAGATTCTTGGAGAAACAGC 480
DB 445 GTGCTGGCTTTCTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGA--- 500

QY 481 ACGAACACAAAGGACTGTGAGCTGCTTTGTTACAGAGTGGTACATCCCTCACCATTACA 540
DB 501 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTCGGAATGGTATACCTTGGCATCACA 558

QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGCTGCTTATTTCAATGATACAGATTAC 600
DB 559 TCAATCTTGAATTCCTGCTTCTGCTGCTTATTTTCAATGATACAGATTATTTAT 618

QY 601 TGGAGCTGTGGAAGCTGTGAGCTGCTCAGTAGGTGCTGAGGCTGCTGAGGCAATTAAT 660
DB 619 TGGAGCTGTGGAAGCTGTGATCTCAGTAGGTGCTGAGGCTGCTGAGGCAATTAAT 678

QY 661 ACTCTTCCAGTGTCTCAGGACATTTACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
DB 679 GTCTCTTCCAACTCTGTGACATCTCATCAGAGGTAGATATCTTCAAGGAGATCTCTT 738

QY 721 CCTGGATTGAAGNATCAGTGTGATCTGTCATCTCAGAAAGTCTTCGAGAAAGAGCAGC 780
DB 739 TCTGATCTGACAGAAAGTCTCTGATCTCTTCAATTCAGAGACAGAGGAGAAAGAGTAGT 798

QY 781 ATCTGTGTCTTAAAGGATCTCATGAAACAGAGATATCTGCTTCAAGTGGGTTC 840
DB 799 CTCAATTTTCTTCAAGAAACAGATGAATAGCAATCAATTTGCTTCAAAATGGGTTC 858

QY 841 TCTGCGATCGGAAAGTGCAGGCTTTCGCCAAAGGAGTAGTACGAGAGCTTCTCAGAGGC 900

DB 859 TTCCTCCCAATCAGATTCGTAGCTCTTCCACAAAGGAACATGTTGAACGTCTTAGAGCC 918
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTTGGCTGGGCTCCA 960
DB 919 AGGAGATTAGCCAAGTCACTGGCCATCTTCTAGGGGTTTGGCTGTTTGGCTGGGCTCCA 978
QY 961 TACTGTCTGTTCAAAATTTGCTTTCAACTTACCCAGAAACGGAAACGCCCCAAATGGGGT 1020
DB 979 TATTCCTCTGTTCAAAATTTGCTTTCAATTTATTTCTCAGCAACAGGCTCTAAATCAGTT 1038
QY 1021 TGGTACAGCAATTTGCTTCTGCTGCAATGGTTCAATTTGTTTAAATCCCTTCTGTAC 1080
DB 1039 TGGTATAGAAATGCAATTTGGCTTCACTTCAATTTCTTGTCAATCTCTTGTAT 1098
QY 1081 CTTTGTGTCAAGCGCTTCCAGAAAGCTTTCTGGAAGATATTTTGTGTGACAAAGCAA 1140
DB 1099 CCAATGTGTCAAGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATAAAAGCAA 1158
QY 1141 CCAGGCTGTCAAGAAC---CAGTCAGTATCTTCTTGA 1176
DB 1159 CCTTACCATCACAACAGTCGGTCAATCTTCTTAA 1197

RESULT 15
US-09-852-165-1
; Sequence 1, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 0023iregus
; CURRENT APPLICATION NUMBER: US/09/852,165
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-165-1

Query Match 58.4%; Score 686.6; DB 10; Length 1300;
Best Local Similarity 75.1%; Pred. No. 2.1e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGCTAAACAGTACTGGCATCTTGCACAGCTGCTCAGGTCCCTTGGCATTT 60
DB 41 ATGCCAGATACCTAATAGCACAACTCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 100

QY 61 TTAATGTCTTCATTTGGCTTTGCTATAATGGTAGCAATGCTGTGTCATCTTACGCCCTTT 120
DB 101 TTTATGCTCTTAGTAGCTTTTGTATAATGCTAGGAATGCTTGGTCAATTTAGCTTTT 160

QY 121 GTGGTGACAGAACTTTAGACATCGAAGTAATTAATTTTTCTTAATTTGGCTATTTCT 180
DB 161 GTGGTGACAGAACTTTAGACATCGAAGTAGTTAATTTTTCTTAACTTTGGGCACTCT 220

QY 181 GACTTCCTCGGGTTTGAATTTCCATTTCTGTACATCCCTCAGGTGTTTAACTGG 240
DB 221 GACTTCCTCGGGTTGATCTCATTCTTGTACATCCCTCAGGTGTTTAACTGG 280

QY 241 AATTTTGGAAAGTGGAAATGCTGATGTTTGGCTCAATTTACTGACTATCTTTTGTGACCGCA 300
DB 281 GATTTTGGAAAGGAAATCTGTTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 340

QY 301 TCTGCTCAGAAATGCTCTCATTAGCTACGATCGATACGATCAGTTCAGTTCATATGCTGTG 360

Db 341 TCTGTATATACATTGTCTCATCAGCTATGATCGATACCTGTGCTCAAAATGCTGTG 400
Qy 361 TCTTATAGGGCTCAACACACTGGGATCATGAGATTTGCTCAAAATGGTGGCTTTGG 420
Db 401 TCTTATAGAACTCAACATCTGGGCTTTGAGATTTGTTACTCTGATGGTGGCCGTTGG 460
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
Db 461 GTGCTGGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTTGGNAGGA---- 516
Qy 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCAACATTACA 540
Db 517 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTCCCATACA 574
Qy 541 ATGCTCTTTGGAAATTCCTGTCTCTGTCTCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db 575 TCAATCTTTGGAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 634
Qy 601 TGGAGCCTGTGAAGCGTAGGGCTCTCAGTAGTGGCTTAGCCATGCTGGATTTCTCCACT 660
Db 635 TGGAGCCTGTGAAGCGTGATCATCTCAGTAGTGGCCAAAGCCATCTTGGACTGACTGCT 694
Qy 661 ACCTCTTCCAGTCTTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAAGTAAT 720
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Db 755 TCTGCATCGACAGAAAGTTCCTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 814
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Db 875 TTCTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAACTGTCTTAGAGCC 934
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Qy 961 TACTGTCTGTTCACAAATGTCTTCAACTTACCCAGAAAGGAAAGCCCAATCGGTG 1020
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Search completed: October 1, 2004, 16:02:43
Job time : 667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 11:11:14 ; Search time 3517 seconds

(without alignments)
9985.193 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atgcggagcttaacagtac.....accagtcagtattctttgga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: em_estov:*

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7: em_estro:*

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9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

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15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

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27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	135.8	11.5	672	14 CB556920	CB556920 AMGNNUC:U
4	133.8	11.4	732	14 CF147822	CF147822 AGENCOURT

5	129.2	11.0	853	14	CD326085	CD326085 AGENCOURT
6	115.6	9.8	684	29	CC481311	CC481311 CH240_309
7	95.99	8.4	643	9	AL848045	AL848045 AL848045
8	95.6	8.1	499	10	BF567596	BF567596 UI-R-B00-
9	88.6	7.5	1046	13	BQ950659	BQ950659 AGENCOURT
10	87.6	7.4	921	29	CNS03296	AL224547 Tetraodon
11	80.6	6.9	754	13	BU468854	BU468854 603373878
12	80.4	6.8	505	13	BQ837058	BQ837058 rf37e04.y
13	80.2	6.8	258	10	AW654609	AW654609 104607 MA
14	78.8	6.7	410	13	BQ836551	BQ836551 rf47c11.y
15	75.8	6.4	523	12	BJ122942	BJ122942 BJT22942
16	75.8	6.4	565	14	CB385348	CB385348 OSTF021G5
17	75.8	6.4	582	12	BU108530	BU108530 BJT08530
18	75.6	6.4	1136	11	BC019470	BC019470 Mus muscu
19	74.8	6.4	562	12	BU103964	BU103964 BJT103964
20	74.8	6.4	566	12	BJ119403	BJ119403 BJT119403
21	74.2	6.3	697	13	BU446363	BU446363 603213444
22	74	6.3	890	12	BI731453	BI731453 603354331
23	73.4	6.2	281	10	BB592940	BB592940 BB592940
24	73.4	6.2	463	9	AU199960	AU199960 AU199960
25	73.4	6.2	602	9	AU207762	AU207762 AU207762
26	73.2	6.2	597	12	BM355525	BM355525 rt26a12.y
27	72.6	6.2	946	13	BQ068856	BQ068856 AGENCOURT
28	72.6	6.2	1103	12	BM548665	BM548665 AGENCOURT
29	72	6.1	701	13	EX851226	EX851226 EX851226
30	70.6	6.0	557	12	BU123503	BU123503 BJT123503
31	70	6.0	875	14	CA472422	CA472422 AGENCOURT
32	68.6	5.8	925	29	CNS021V9	AL177390 Tetraodon
33	68.6	5.8	1050	29	CNS02GPD	AL196618 Tetraodon
34	68.4	5.8	1037	29	CNS022VG	AL178693 Tetraodon
35	67.6	5.7	889	14	CB565881	CB565881 AGENCOURT
36	67	5.7	1770	29	AY400784	AY400784 Mus muscu
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39	66.4	5.6	281	29	CE291362	CE291362 tigr-gss-
40	66	5.6	795	14	CD804122	CD804122 UI-M-GV0-
41	66	5.6	3816	11	AK081248	AK081248 Mus muscu
42	64.4	5.5	821	14	CB565878	CB565878 AGENCOURT
43	64	5.4	465	12	BI510489	BI510489 BB170001A
44	63.6	5.4	910	10	BE783826	BE783826 601471053
45	63.2	5.4	355	12	BU107479	BU107479 BJT07479

ALIGNMENTS

RESULT 1	BX643713	839 bp	mrna	linear	EST 04-SEP-2003
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ACCESSION	BX643713				
VERSION	EST.				
KEYWORDS	EST.				
SOURCE	BX643713.1	GI:34478046			
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 839)				
AUTHORS	Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M. and Wiemann S.				
TITLE	EST (Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., et al.)				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: MIPS				
	MIPS				
	Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany				
	This is the 5' sequence of the clone insert				
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;				
	consortium of the German Genome Project.				
	No sl sequence available.				
	This clone (DKFp781C0629) is available at the RZPD in Berlin.				

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 839

FEATURES

source
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZp781C0629"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB; cDNA collection"

ORIGIN

Query Match 37.3%; Score 438.6; DB 13; Length 839;
Best Local Similarity 75.9%; Pred. No. 7.7e-100;
Matches 570; Conservative 0; Mismatches 174; Indels 7; Gaps 2;

QY 1 ATGTCGGAGCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTT 60
DB 96 ATGCCAGATACCTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 155
QY 61 TTAATGCTCTTCAATTTGGCTTCTATATATGTTAGGCAATGCTGTGGTCACTTTAGCCCTTT 120
DB 156 TTATGCTCTTGTAGTCTTTGCTATATGCTAGGAATGCTTTGGTCACTTTAGCTTTT 215
QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAAATATTTTTTCTTAATTTGGCTATTCT 180
DB 216 GTGTGGACAGAAACCTTAGACATCGAAGTAAATATTTTTTCTTAATTTGGCTATTCT 275
QY 181 GACTTCTCTGTTGGTTGATTTCCATCTCTGTACATCCCTCAGCTGTGTTAACTGG 240
DB 276 GACTTCTTGTGGGTGATCTCCATCTCTTTGTACATCCCTCAGCTGTGTTAACTGG 335
QY 241 AATTTTGAAGTGGAAATCTGATGTTTGGCTCAITACTGACTATCTTTTGTGCACCGCA 300
DB 336 GATTTTGAAGAAATCTGATGTTTGGCTCAITACTGACTATCTTTTGTGCACCGCA 395
QY 301 TCTGTCTACAATATTGCTCTAATAGTACGATACGATACGATACGATACGATACGATACG 360
DB 396 TCTGTATATAACATTTGCTCTATCATGATATGATGATGATGATGATGATGATGATGATG 455
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAGATGTTGCTCAATGTTGGTGTGCTTTGG 420
DB 456 TCTTATAGAACTCAACATCTGGGCTCTTGAAGATTTGTTACTCTGATGTTGGCTTTGG 515
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGGAGAACAGC 480
DB 516 GTGCTGGCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAGGA--- 571
QY 481 AGAACACAAAGACTGTGAGAGCTGGCTTTGTACAGAGTGTGTACATCTCCACATTACA 540
DB 572 --TGAAGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTGTACATCTTGGCATACA 629
QY 541 ATGCTCTTGAATTTCTGCTTCTCTGTCATCTGTCGCTTTATTTCAATGTACAGATTTAC 600
DB 630 TCAATCTTGAATCTGATGATCCAGTCACTTTAGTCTGCTTTATTTCAACATGATTTAT 689
QY 601 TGGAGCTGTGGAAGGCTAGGCTCTCAGTAGTGTGCTTAGCCATGCTGGATTTCTCCACT 660
DB 690 TGGAGCTGTGGAAGGCTGATCATCTCAGTAGTGTGGAAGGCTCTGCTGACTGCTCT 749
QY 661 ACTCTTTCAGTCTTCAGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
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QY 721 CTTGGATTGAAGAAATCAGCTGATCTGTC 751
DB 809 TCTGCTGACAGAAAGTCTCTGATCTTTC 839

RESULT 2

CF147821

LOCUS

DEFINITION

AGENCOURT 14740195 NIH MGC 145 Homo sapiens cDNA clone

IMAGE:6971900 5', mRNA sequence.

ACCESSION

CF147821

VERSION

CF147821.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (Bases 1 to 704)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBI02 row: b column: 07

High quality sequence stop: 685.

Location/Qualifiers

1..704

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6971900"

/tissue_type="mixed"

/lab_host="DH10B"

/clone_lib="NIH MGC 145"

/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:

varies by clone; ORFs were PCR-amplified and cloned into

pcDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XbaI/XhoI-3',

5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat

a Note: this is a NIH_MGC Library."

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ORIGIN

Query Match 11.4%; Score 133.8; DB 14; Length 732;
Best Local Similarity 53.5%; Pred. No. 7.3e-23;
Matches 329; Conservative 0; Mismatches 277; Indels 9; Gaps 2;
QY 3 GTCGAGTCTAACAGTACTGGCACTTCCACAGCTGCTCAGTCCCTTGGCATTTT 62
DB 76 GCGCGCGCGCGCGCGCGCTTCTCGCAGCTGCGACCGCGGTGCGCGCGCT 135
QY 63 AATGCTTCATTGCTTGTATATAGTGTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122
DB 136 CATGCGCTGCTCATGTTGGCAGCGTCTGGCAACGCGTGTGCTGCTCGCTTGT 195
QY 123 GGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTTCTTAATTTGGCTATTCTGA 182
DB 196 GCGGACTCGAGCTCCGACCCAGCAACAATCTTCTCTGCTCAACCTCGCATCTCGA 255
QY 183 CTTCCTGCTGGTTGATTTCATTCCTCTGTACATCCCTCACGTTG---TTTAACTG 239
DB 256 CTTCCTGCTGGCGCTTCTGCACTCCACTGTATGACCTTACCTGCTGACAGCGCTG 315
QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCAATTAAGTACTATCTTTTGTGACCGC 299
DB 316 GACCTTCGCGCGCGCTCTGCAAGCTGTGCTGTAGTGAATCTGCTGTGACCTC 375
QY 300 ATCTGCTACAAATTTGCTCATTAGTACGATACATACAGTCAAGTTTCAAACTGT 359
DB 376 CTCTGCTTCAACATCGTCTCATCAGCTACGACGCTTCTCTGCTGCGTCAACCGAGCGT 435
QY 360 GTCTATAGGCTCAACACATCGGATCATGAGATTGTTGCTCAAAAGTGGCTGTTG 419
DB 436 CTATACCGGCGCGCGCTGACACGCGCGCGAGTGCAGAGATGCTGCTGTGTG 495
QY 420 GATCTGGCTTCTTGGTAAATGGCGCGATGTTCTGGCTTCAGA-----TTCTTGAA 473
DB 496 GTGTGCTGGCTTCTGCTGTACGACACCATCTGAGCTGGAGTACTCTGCGGGG 555
QY 474 GAACAGCAGCAACACAAAGACTGTGAGCTGGCTTTGTTGACAGAGTGTATCTCAC 533
DB 556 CAGCTCCATCCCGAGGCGCACTGTATGCCAGTTCCTTCTACAACTGTACTTCTCAT 615
QY 534 CATTACAATGCTTTGGAATCTGCTTCTGCTCATCTGCTGCTTATTTCATGTACA 593
DB 616 CACGGCTCCCACTGGAGTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAC 675
QY 594 GATTACTGGAGCT 608
DB 676 CATCTACCTGAACAT 690

RESULT 5

CD326085 853 bp mRNA linear EST 28-MAY-2003
LOCUS AGENCOURT 14163426 NICHG_XGC_Eyel Xenopus laevis cDNA clone
DEFINITION IMAGE:6949081 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD326085.1 GI:31090416

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 853)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14564 row: f column: 24

High quality sequence stop: 707.

Location/Qualifiers

FEATURES

source

1..853

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:6949081"

/dev_stage="adult"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NICHG_XGC_Eyel"

/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 2.3 kb. Constructed by Life

Technologies. Note: This is a Xenopus Gene Collection

(XGC) library."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

0

Mismatches

168

Indels

3

Gaps

1;

QY 45 GGTCCCTTGGCAATTTAATGCTTCAATTTGCCCTTGTCTAATAATGGTAGGAATGCTGT 104

DB 381 GGTCTTCTGGCTGTCTGATGGGGTCTCTCATAGTTAGCACCGTCTGGGAATGCCCT 440

QY 105 GGTCACTTAGCTTTGTGCTGGACAGAACTTACATCGAAGTAATTTATTTTCT 164

DB 441 GGTCACTAGCTTTGTGCTGGACTCCAGCTCCGACCCAGAAATTAATTTCTCTTCT 500

QY 165 TAATTTGGCTATTCTGACTTCTCGTGGTGTGATTTCCATTCTCTGTACATCCCTCA 224

DB 501 CAACCTGGCTATCTCAGATTTCTTTGTAGTCCCTGTGCATCCCTCTGTATGGCATA 560

QY 225 CGTGTGTTT---AACTGGAATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTAATGA 281

DB 561 CGTACTGACTGCGAGATGAGCTTTGGCAGAGCGTTTGCAGCTGTGGCTGGTCTGGA 620

QY 282 CTATCTTTTGCACCGCATCTCTACAATATTTGCTCATTTAGCTACGATCGATACCA 341

DB 621 TTATCTGCTCGACCTCGTCCGTGTTCAACATCGTGTCTCATCAGCTACGACAGTTT 680

QY 342 GTCAGTTTCAAAATGCTGTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGC 401

DB 681 CTCTGTGACCGGGCTGTGATACCGAGCTCAGAGAGTAACAGCGGCGATCGACTTT 740

QY 402 TCAAAATGGTGTGTTTGGATGACTGCTTTCTTGTAAATGGCCCATGTTCT 455

DB 741 GAAATGACCATGGTGTGGATCTTGGCTTTCTCTATATGGACCACCATTAAT 794

RESULT 6

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

CC481311

Bos taurus

CH240_309C10.77 CHORI-240 Bos taurus genomic clone CH240_309C10,

genomic survey sequence.

CC481311

Bos taurus

CC481311.1 GI:31760574

GSS.

Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 684)

CC481311 684 bp DNA linear GSS 16-JUN-2003

CH240_309C10.77 CHORI-240 Bos taurus genomic clone CH240_309C10,

genomic survey sequence.

CC481311

Bos taurus

CC481311.1 GI:31760574

GSS.

Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 684)

AUTHORS

Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Gira, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., We, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B. P., and Tellam, R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_309C10.TARBAC13P2
Contact: Rob Holt

TITLE

JOURNAL

COMMENT

Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Plate: 309 row: C column: 10

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..684

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="bred: Hereford"

/db_xref="taxon:9913"

/clone="CH240_309C10"

/sex="Male"

/cell_type="Blood"

/clone_lib="CHORI-240"

/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;

Hereford bull L1 Dominio 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 9.8%; Score 115.6; DB 29; Length 684;
Best Local Similarity 70.6%; Pred. No. 2.8e-18;
Matches 154; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 150 TAATTATTTTCTTAATTGGCTATTTCTGACTTCTCGTGGGTTTGATTCCTCCATTC 209
DB 260 TAGGTGCTATATTGTAAATCTTCAATTTTTCGCCCATGCGAGGTATGATCTCCATTC 319

QY 210 TCTGTACATCCCTCACGCTGTTGTTAACTCGMAATTTTGGAGTGGATCTGCATGTTTG 269
DB 320 TTTATTCATCCCTCACAGCTCTTCAACTGGAGTTTGAATAAATTAACATTTGTGCTTTTG 379

QY 270 GCTCAATPACTGACTATCTTTTGTGACCGCATCTGTCTACAATATGTCCTCAATAGCTA 329
DB 380 GCTCACTACTGACTATCTTTTGTGTACAGCATCTGTGTATTAACATCTACTCATCAGCTT 439

QY 330 CGATCGATACAGTCAAGTTCATTAATGCTGTGCTTATA 367
DB 440 TGATCGATATCAGTCACTGCTCCAATGCTGTAAGTCAAA 477

RESULT 7

AL848045

LOCUS

AL848045 XGC-egg Silurana tropicalis 643 bp mRNA linear EST 26-NOV-2003
sequence.

ACCESSION

AL848045

VERSION

AL848045.2

KEYWORDS

EST.

SOURCE

Silurana tropicalis

ORGANISM

Silurana tropicalis (western clawed frog)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Silurana.

1 (bases 1 to 643)

Sanger Xenopus tropicalis EST project 2001 (11_2003)

Unpublished (2003)

Contact: Taylor R

On Sep 15, 2002 this sequence version replaced gi:22868310.

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: TEGG022122.plkSP6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with EORI at the

5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EORI; Site 2: NotI

Host: Escherichia coli XL1-blue.

Location/Qualifiers

1..643

/organism="Silurana tropicalis"

/mol_type="mRNA"

/db_xref="taxon:9364"

/clone="TEGG022122"

/dev_stage="egg"

/lab_host="Escherichia coli XL1-blue"

/clone_lib="XGC-egg"

/note="Vector: pCS107; Site 1: EORI; Site 2: NotI; cDNA

was oligo dT primed from 5ug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with

ECORI at the 5' end and NotI at the 3' end"

ORIGIN

Query Match 8.4%; Score 99; DB 9; Length 643;
Best Local Similarity 55.5%; Pred. No. 4.4e-14;
Matches 236; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

QY 193 GGTGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTT---AACTGGAATTTGGA 249
DB 83 GTGGGATTCGATCCCACTCTATATCCCTTATGTGCTGACTGCGCCAGTGGAGTTGGG 142

QY 250 AGTGGAAATCGCATGTTTGGCTCATCTACTGACTATCTTTTGTGACCGCATCTGTCTAC 309
DB 143 AAAGGCTTGCGAAGTTGTGCTAGTAGTAATGAGTACCTTTTATGCACTGCTTCAGTTT 202

QY 310 AATATTGCTCTATTAGTACGATCGATACGATCCAGTTCAGTTTCAAATGCTGTGCTTATAGG 369
DB 203 AATATTGCTCTATCAGTATGACAGGTTTCATCTCAGTCACTAAAGCGGTGCTCTACAGA 262

QY 370 GCTCAACACACTGGCATCATGAAGATGTTGCTCAATGGTGGCTGTTTGGACTACTGGCT 429
DB 263 GCACAGAAAGGAATGACAGAAATGACAGTGTAAATGCTTATTTGTTGGTGGCAGCC 322

QY 430 TTCTTGTAATAGGCCCGATGATTCTGGCTTCAGA-----TTCTTGGAAAGAACAGCAGC 483
DB 323 TTCTTCTCTATGCCCCAGCCATCATCACCTGGGAATACATTGCAAGAACTACTATCTTAA 382

QY 484 AACACAAAGGACTGTGAGCGCTGCTTTGTTTACAGAGTGGTACATCTCTCAATTCACATG 543
DB 383 CCAGAAAGGGGAATGTTATGTAGAATTTCTACTACAACTGGTATTTTCTGATGATAGCTTC 442

QY 544 CTCTTCGAATTCCTGCTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTACTGG 603
DB 443 ACAATAGAATCTTTTACTCCATTCATCAGTGTTCCTATTTTCAATCTAAGCATCTACAT 502

QY 604 AGCCT 608
DB 503 AACAT 507

RESULT 8
BF567596 499 bp mRNA linear EST 12-DEC-2000
LOCUS UI-R-B00-agr-c-06-0-UI.r1 UI-R-B00 Rattus norvegicus cDNA clone
DEFINITION UI-R-B00-agr-c-06-0-UI 5', mRNA sequence.
ACCESSION BF567596
VERSION BF567596.1 GI:11677326
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 499)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PubMed 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEHRR, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1796445
Seq primer: M13 Forward

FEATURES
source

1..499
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B00-agr-c-06-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-B00"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratseq.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Query Match 8.1%; Score 95.6; DB 10; Length 499;
Best Local Similarity 54.5%; Pred. No. 3e-13;
Matches 238; Conservative 0; Mismatches 190; Indels 9; Gaps 2;
QY 192 GGGTTTGATTCCATTCCTCTGTACATCCCTCAGCTGTGTTTAAAC---TGGAAATTTGG 248
Db 58 GGGTGCCCTTCGATCCCATTTGATAGTACCTATGCTGACCGCGCGTGGACCTTCGG 117
QY 249 AAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTTGTGACCGCATCTGCTA 308
Db 118 CCGGGGCTCTGAAGCTGTGGCTGGTGGTAGACTACTACTGTGTGCCCTCCCTGGGCTT 177
QY 309 CAATATTGCTCTATTAGTACGATACGATACAGTTCAGTTTCAAATGCTGTGTTATAG 368
Db 178 CAATCGTACTCATAGCTATGACCAATTCCTGTAGTCACTCGACTGTCTCCACAG 237
QY 369 GGCTCAACACATGGCATCATGAAGATTGTTGCTCAAAATGGTGCTGTTGGATCTGGC 428

Db 238 GGGCCAGCAGGGGGACACGAGACGGCGCTTGGGAAGATGGCACTGGTGTGGGTCTGGC 297
QY 429 TTCTTTGTAATAATGCCCGGATGATTCTGGCTTCAG-----TTCTTGAAGAAGACAGCAC 482
Db 298 CTTCCTGTGTATAGGGCCCTGCATCTCCTAGTTGGAGTACCTGTCTGGTGGCAGTTCCAT 357
QY 483 GAACACAAAGGACTGTGAGCCCTGGCTTTGTGTACAGAGTGGTACATCTCCACCATTAACAT 542
Db 358 CCCGAGGGCCACTGCTATGTGAGTTCTTCTACAACTGGTACTTCTCATCAGCGNCTC 417
QY 543 GCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTCAATGTACAGATTACTG 602
Db 418 CACCCTCGAGTTCTTACGCGCCCTTCTCAGCGTTACCTTCTTCAACCTCAGCATCTACCT 477
QY 603 GAGCCTGTGGAGCGTA 619
Db 478 GAACATCCAGAGCGCA 494

RESULT 9

BQ950659 1046 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT_8863943 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311932
DEFINITION 5', mRNA sequence.
ACCESSION BQ950659
VERSION BQ950659.1 GI:22366137
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1046)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13736 row: k column: 05
High quality sequence stop: 640.

FEATURES
source

1..1046
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6311932"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 7.5%; Score 88.6; DB 13; Length 1046;
Best Local Similarity 61.6%; Pred. No. 2e-11;
Matches 141; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 238 TGAATTTTGAAGTGAATCTGATGTTTGGCTCATTACTCACTATCTTTGTGCACC 297
Db 488 TGAACCTTTGGCGGGCCCTCTCAAGCTGTGCTGGTGGTAGACTACTTGTGTGCC 547
QY 298 GCATCTGTCTACAAATATTGTCCTCAATTAGCTAGCATGATACCAGTCAGTTTCAAATGCT 357
Db 548 TCCTCAGTCTTCAACATCGTGTGCTGATCAGCTATGACCGATTCTCTGTGCTCAGTCTGAGCT 607

Qy	358	GTGTCATTATAGGGCTCAACACACTGGGCATCAATGAAGATTGTGTCTCAAAATGGTGCTGTT 411
Db	608	GTCTCTCTACCGGGCCAGCAGCGGGGACACAAGACGGGCTGTTTCGAAAGATGCACCTGGTG 667
Qy	418	TGGATACCTGGCTTTCTTGGTAAATGGCCCGATGATTCCTGGCTTCAGATT 466
Db	668	TGGGTGCTGGCTTCTGCTGTATGGGCTCGGCATCTCTGAGTTGGAGT 716
RESULT 10		
CNS03296/c		
LOCUS	CNS03296	921 bp DNA linear GSS 01-SEP-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 26D09 of library G from tetraodon nigroviridis, genomic survey sequence.	
ACCESSION	AL224547	
VERSION	AL224547.1	GI:7883412
KEYWORDS	GSS; genome survey sequence.	
SOURCE	Tetraodon nigroviridis	
ORGANISM	Tetraodon nigroviridis	
REFERENCE	1 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.	
AUTHORS	Roest Crolius,H., Jaillon,O., Basilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.	
TITLE	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence	
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)	
MEDLINE	20296633	
PUBMED	10835645	
REFERENCE	2	
AUTHORS	Roest Crolius,H., Jaillon,O., Pasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.	
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	
JOURNAL	Genome Res. 10 (7), 939-949 (2000)	
MEDLINE	20359837	
PUBMED	10899143	
REFERENCE	3 (bases 1 to 921)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr	
COMMENT	- Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	
FEATURES	Location/Qualifiers	
source	1..921	
	/organism="Tetraodon nigroviridis"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:99883"	
	/clone="206D09"	
	/clone_lib="G"	
	/note="Genoscope sequence ID : COAG206CH051P1-end : T7"	
ORIGIN		
Query Match	7.4%	Score 87.6; DB 29; Length 921;
Best Local Similarity	59.0%	Pred. No. 3.5e-11;
Matches 170; Conservative	0; Mismatches 114; Indels 4; Gaps 1;	
Qy	889	CTTCTCAGAGCGAGAGCTAGCAGGTCTACTGGCCATCTCTTCGACGCGTTTTCGCATT 948
Db	588	CTGTCCAGACACAAAAGATTGCGCAATCTCTGGCCATTATCGTCTGTATTTTCGGGATC 529
Qy	949	TGCTGGGCTCCACTACTGTCGTTCACAAATGTCTCTTCAACTTACCCAGACGGAACGC 1008

Db 528 TGTGGGCCCCCTACACGCTGCTGATGATCATCGCGCGCGCTCGACGGCGAGGTGGTGG 469
 Qy 1009 CCCAAATCGGTGGTACACGATTCCTTGGCTGCAATGGTTCAATTCGTTGTTAAAT 1068
 Db 468 CCGACTAC-----TGGTAAGAGATAA CTTCTGGCTCTGTGGCTCACTCAGCCATCAAC 413
 Qy 1069 CCCTTTCTGTACCCCTTTGTGTCTACAGCGTTTCCAGAGGCTTCTGTGGAAGATACATTTGT 1128
 Db 412 CCCTTCTGTGTACCGCGTGTGCCACAGCAGCTTCGGAGGGCTTCTCCAGATCCCTGTGT 353
 Qy 1129 GTGACAAGCAACACCGCGTGTACAGACACAGCTAGTATCTTCTTGA 1176
 Db 352 CCCAAAGACAGTCGGTTCAGCCTCAGATCGAAGTCCAGTCGTGTAA 305

RESULT 11
 BU468854
 LOCUS 603373878F1 CSQRBN20 Gallus gallus cdna clone CHEST284119 5', mRNA
 DEFINITION sequence.
 ACCESSION BU468854
 VERSION BU468854.1 GI:25962431
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 754)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken CDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..754
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST284119"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate
 cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSQRBN20"
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI;
 Site 2: NotI; This normalized library was constructed from
 1 million independent clones. cDNA synthesis was initiated
 using an oligo(dT) primer, using methylated C in the first
 strand synthesis reaction. Following this first strand
 reaction, double-stranded cDNA was blunted, ligated to
 NotI adapters, digested with EcoRI, size-selected, and
 cloned into the NotI and EcoRI compatible sites of a
 custom modified MCS of the pBluescript (KS+) vector. The
 library was normalized in 2 rounds using conditions
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
 Bonaldo et al., Genome Research 6 (1996): 791, except that
 a significantly longer reannealing hybridization was
 used."

ORIGIN
 Query Match 6.9%; Score 80.6; DB 13; Length 754.

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

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ORIGIN
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Best Local Similarity 59.1%; Pred. No. 2.1e-09;
Matches 136; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 237 CTGGAATTTTGAAGCTGGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGTGCAC 296
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4 CTGGCCCTTCGCCCGGGCCCTCGAAGCTGTGGTGGCGGACTACCTCTCTGCCC 63

QY 297 CGCATCTGTCTACAATATTGCTCCTCATTAGCTACGATCGATACCACTAGTTCAGTTTCAAATGC 356
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64 CTCCTCTGTCTCATATCGCGCTCATCAGCTATGACCGCTTCCTGTGCGNACCCGAGC 123

QY 357 TGTGCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGTCAAATGGTGGCTGT 416
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
124 GGTCTCTACCGGACCCAGCGGTGACACGGCGCGCGAGAGATGGTCTGT 183

QY 417 TTGGATCTGGCTTCTTGGTAAATGGCCCGCATGATTCTGGCTTCAGATT 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 GTGGTGTGGCTTCTCTGTATGGACCCCGCATCTCAGTTGGAGT 233

RESULT 14
BO836551
LOCUS rf47c11.y1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5',
similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ;, mRNA sequence.
ACCESSION BO836551
VERSION BO836551.1 GI:22140865
KEYWORDS EST.
SOURCE Meloidogyne hapla
ORGANISM Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.
REFERENCE 1 (bases 1 to 410)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schuck,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,N., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
TITLE Contact: McCarter JP
JOURNAL The Washington Univ. Nematode EST Project, 1999
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone will not be made available due to an unidentified
microbial contamination of the source material.
Seq primer: -40RP from Gibco.
FEATURES
source
1. .410
/organism="Meloidogyne hapla"
/mol_type="mRNA"
/db_xref="taxon:6305"
/dev_stage="J2"
/lab_host="DH10B"
/clone_lib="Meloidogyne hapla J2 pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. J2 were provided by Dr. Valerie
```

Williamson of the University of California at Davis
(vmwilliamson@ucdavis.edu)."

```
ORIGIN
Query Match      6.7%; Score 78.8; DB 13; Length 410;
Best Local Similarity 55.0%; Pred. No. 5.1e-09;
Matches 177; Conservative 0; Mismatches 142; Indels 3; Gaps 1;

QY 53 TGGCAATTTTAAAGTCTCAATTTGGCTTTGCTATATAGGTAGCGCAATGCTGGTCACT 112
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
21 TTGTAATATTGGATTATTTTCTCATTAGCTACACGATCGGAATGCTCTTGTATGC 80

QY 113 TAGCCTTTGTGGACAGAACCTTAGACATCGAAGTAATTTTCTTAAATGG 172
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 TTCTATTGTGTGATATAAAATACAAACAATTAGCAATTAATTTCTTTCTCTTAG 140

QY 173 CTATTTCTGACTTCCTCGTGGGTTTGATTTCATTCCTCTGTACATCCCTCACGTTGT 232
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
141 CTGTTGCTGATCTACTATTGGCTTATTTCTATTCCTCTTATGACTTTATATACGGCA 200

QY 233 TTAACT---TGGAAATTTGGAAGTGAATCTGCANGTTTTGGCTCAATTAATGATCTTT 289
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 ATGAGACTTGGACTTTTGGTTATCTCTTTGTCAATTCGGCTCTGTATAGATTATTAA 260

QY 290 TGTGACCGCATCTGCTACAAATATTGCTCCTCATTAGCTACGATCGATACCACTT 349
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
261 TGTGCATGCTTCAGCACTCAATTTGTTATTAAATTAGCTTTGATAGATACTTTCTGTTA 320

QY 350 CAAATGCTGTCTTATATAGGGC 371
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
321 CCCGACCTTTAACTTACAGGCC 342

RESULT 15
BJ122942
LOCUS BJ122942
DEFINITION BJ122942 523 bp mRNA linear EST 23-JAN-2002
Caenorhabditis elegans cDNA library, C. elegans L1 stage
ACCESSION BJ122942
VERSION BJ122942.1 GI:18283081
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 523)
AUTHORS Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
TITLE Contact: Tadasi Shin-i
JOURNAL Center For Genetic Resource Information
COMMENT National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1. .523
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1293h04"
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/tissue_type="whole animal"
/dev_stage="L1"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 13:54:44 ; Search time 4880 Seconds
(without alignments)
10444.961 Million cell updates/sec

Title: US-10-626-445-5
Perfect score: 1176
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
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- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1176	100.0	1538	10	AF358859	Mus muscu
C	819	69.6	200346	2	AC131672	AC131672 Mus muscu
3	67	5.7	1593	10	AF358860	AF358860 Rattus no
C	4	5.7	236694	2	AC118386	AC118386 Rattus no
5	28	2.4	1291	4	AB053300	AB053300 Sus scrof
6	26	2.2	1451	10	AF358858	AF358858 Cavia por
7	22	1.9	223	6	AX775381	AX775381 Sequence
8	22	1.9	849	11	BV056167	BV056167 S212P6390
9	22	1.9	1173	6	AR142850	AR142850 Sequence
10	22	1.9	1173	6	AR391860	AR391860 Sequence
11	22	1.9	1173	6	AX109119	AX109119 Sequence
12	22	1.9	1173	6	AX139113	AX139113 Sequence
13	22	1.9	1173	6	AX301763	AX301763 Sequence
14	22	1.9	1173	6	BD015847	BD015847 Novel pol
15	22	1.9	1173	9	AF307973	AF307973 Homo sapi
16	22	1.9	1173	9	AF325356	AF325356 Homo sapi
17	22	1.9	1173	9	AF329449	AF329449 Homo sapi
18	22	1.9	1173	9	AY008280	AY008280 Homo sapi
19	22	1.9	1173	9	AI136745	AI136745 Homo sapi
20	22	1.9	1173	9	BD097512	BD097512 Novel gua
21	22	1.9	1227	6	BD097512	BD097512 Novel gua
22	22	1.9	1265	9	AB044934	AB044934 Homo sapi
23	22	1.9	1266	6	AX376577	AX376577 Sequence
24	22	1.9	1300	6	AX301229	AX301229 Sequence
25	22	1.9	1312	6	BD095598	BD095598 Novel gua
26	22	1.9	1312	9	AB045370	AB045370 Homo sapi
27	22	1.9	3689	6	AX549343	AX549343 Sequence
C	28	1.9	3689	9	AF312230	AF312230 Homo sapi
29	22	1.9	91811	10	AL670670	AL670670 Mouse DNA
C	22	1.9	140555	9	AC007922	AC007922 Homo sapi
30	22	1.9	168206	2	AC009668	AC009668 Homo sapi
C	22	1.9	167296	2	AF002507	AF002507 Homo sapi
31	22	1.9	169144	9	AC090244	AC090244 Homo sapi
C	22	1.9	184938	2	AP002476	AP002476 Homo sapi
32	22	1.9	193779	2	AP001327	AP001327 Homo sapi
C	22	1.9	229392	2	AC112372	AC112372 Rattus no
33	22	1.9	255561	2	AC121624	AC121624 Rattus no
C	21	1.8	358	4	AB060079	AB060079 Oryctolag
34	21	1.8	505	9	AF435588	AF435588 Homo sapi
35	21	1.8	696	6	AX677239	AX677239 Sequence
36	21	1.8	867	6	AR026630	AR026630 Sequence
37	21	1.8	1050	6	FI2845	FI2845 cDNA encodi
38	21	1.8	1250	9	AB029932S2	AB029933 Homo sapi
39	21	1.8	7019	9	AB009811	AB009811 Homo sapi
40	21	1.8	62240	2	AC100874	AC100874 Homo sapi
41	21	1.8	62240	2	AC100874	AC100874 Homo sapi

ALIGNMENTS

RESULT 1
AF358859
LOCUS AF358859 1538 bp mRNA linear ROD 02-SEP-2001
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358859
VERSION AF358859.1 GI:15420534
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 1538)
TITLE Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation

JOURNAL	Unpublished	
	2. (bases 1 to 1538)	
REFERENCE	Liu, C., Wilson, S., Kuei, C. and Lovenberg, F. W.	
AUTHORS	Direct Submission	
TITLE	Submitted (12-MAR-2001) Molecular Pharmacology, The R. W. Johnson	
JOURNAL	Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA	
FEATURES	Location/Qualifiers	
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ORIGIN	Query Match 100.0%; Score 1176; DB 10; Length 1538;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Qy	61 ATGTGGAGCTTAACAGTACTGCGATCTTCCACACAGCTGCTCAGTCCCTTGGCATTT 120	
Db	61 TTAATGCTTCATTTCGCTTTGTATAATGTTAGGCAATGCTGTGGTCATCTTAGCCTTT 120	
Qy	61 TTAATGCTTCATTTCGCTTTGTATAATGTTAGGCAATGCTGTGGTCATCTTAGCCTTT 120	
Db	121 TTAATGCTTCATTTCGCTTTGTATAATGTTAGGCAATGCTGTGGTCATCTTAGCCTTT 180	
Qy	121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180	
Db	181 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 240	
Qy	181 GACTTCCTGTGGTTGATTTTCATCTCTGTACATCCCTCAGCTGTTTAACTGG 240	
Db	241 GACTTCCTGTGGTTGATTTTCATCTCTGTACATCCCTCAGCTGTTTAACTGG 300	
Qy	241 AATTTTGAAGTGGAACTCTGCATGTTTGGCTCATTAAGTATCTTTTGTGACCGCA 300	
Db	301 AATTTTGAAGTGGAACTCTGCATGTTTGGCTCATTAAGTATCTTTTGTGACCGCA 360	
Qy	301 TCTGTCTACAAATATGTCTCAATAGTACATGATGATGATGATGATGATGATGATG 360	
Db	361 TCTGTCTACAAATATGTCTCAATAGTACATGATGATGATGATGATGATGATGATG 420	
Qy	361 TCTTATAGGCTCAACACATGATGATGATGATGATGATGATGATGATGATGATGATG 420	
Db	421 TCTTATAGGCTCAACACATGATGATGATGATGATGATGATGATGATGATGATGATG 480	
Qy	421 ATACTGCTTCTTGTGTAATGTCGCGATGATGATGATGATGATGATGATGATGATG 480	
Db	481 ATACTGCTTCTTGTGTAATGTCGCGATGATGATGATGATGATGATGATGATGATG 540	
Qy	481 ACGAACCAAGAGCTGTGAGCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 540	
Db	541 ACGAACCAAGAGCTGTGAGCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 600	
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Db	601 ATGCTCTTGAATTCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660	
Qy	601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCGCTCAGTAGGTGCGCTCAGT 660	

----- Project Information -----
 Center project name: M BA0314021
 ----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 199211 bases at least Q40
 Consensus quality: 199561 bases at least Q30
 Consensus quality: 199715 bases at least Q20
 Insert size: 199000; agarose-fp
 Insert size: 199990; sum-of-contigs
 Quality coverage: 13.37 in Q20 bases; agarose-fp
 Quality coverage: 11.03 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 56: contig of 56 bp in length
 * 57 156: gap of unknown length
 * 157 1270: contig of 1114 bp in length
 * 1271 1370: gap of unknown length
 * 1371 85906: contig of 84536 bp in length
 * 85907 86006: gap of unknown length
 * 86007 200346: contig of 114340 bp in length.

FEATURES

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misc_feature	86007. 200346	/note="assembly_name:Contig17"	
ORIGIN			
Query Match	69.6%; Score 819; DB 2; Length 200346;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 819; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	358 GTGCTTATAGGCTCAACACACATGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTT	417	
Db	93719 GTGCTTATAGGCTCAACACATGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTT	93660	
QY	418 TGGATACCTGGCTTTCTTGGTAAAGGCCCGCATGATCTGGCTTCAGATTCTTGGAGAAC	477	
Db	93659 TGGATACCTGGCTTTCTTGGTAAAGGCCCGCATGATCTGGCTTCAGATTCTTGGAGAAC	93600	
QY	478 AGCAGAACACAAAGGACTGTGAGCCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATT	537	
Db	93599 AGCAGAACACAAAGGACTGTGAGCCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATT	93540	
QY	538 ACAATGCTCTTGGAAATCTCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATT	597	
Db	93539 ACAATGCTCTTGGAAATCTCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATT	93480	
QY	598 TACTGGAGCCTGTGGAGCGTAGGGCTCTAGTAGTGGCCCTAGCCATGCTGGATTCTCC	657	
Db	93479 TACTGGAGCCTGTGGAGCGTAGGGCTCTAGTAGTGGCCCTAGCCATGCTGGATTCTCC	93420	

QY	658	ACTACCTCTTCAGTGCTTCAGGACACTTACACAGAGCTGGGCTGGCTTCGAGGACAACT	717
Db	93419	ACTACCTCTTCAGTGCTTCAGGACACTTACACAGAGCTGGGCTGGCTTCGAGGACAACT	93360
QY	718	AATCTGGATTGAAGGAATCAGCTGTCATCTCGTCACTCAGAAAGTCTCGAAGAAGAGC	777
Db	93359	AATCTGGATTGAAGGAATCAGCTGTCATCTCGTCACTCAGAAAGTCTCGAAGAAGAGC	93300
QY	778	AGCATCTGGTGTCTTAAAGACTCACAATGAACAGCAGTATCATCTGCTTCAAGTGGGT	837
Db	93299	AGCATCTGGTGTCTTAAAGACTCACAATGAACAGCAGTATCATCTGCTTCAAGTGGGT	93240
QY	838	TCCTTCTGGCCATCGGAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGCTTCTCAGA	897
Db	93239	TCCTTCTGGCCATCGGAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGCTTCTCAGA	93180
QY	898	GGCAGGAAGCTAGCCAGCTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGCT	957
Db	93179	GGCAGGAAGCTAGCCAGCTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGCT	93120
QY	958	CCATCTGTCTGTTCACAATTTGCTTCACTTACCCAGAACGGAAACGCCCCCAATCG	1017
Db	93119	CCATCTGTCTGTTCACAATTTGCTTCACTTACCCAGAACGGAAACGCCCCCAATCG	93060
QY	1018	GTGTGGTACAGCATTTGCTGCTGCAATGGTTCAATTCGTTGTTAATCCCTTCTG	1077
Db	93059	GTGTGGTACAGCATTTGCTGCTGCAATGGTTCAATTCGTTGTTAATCCCTTCTG	93000
QY	1078	TACCTTTGTCTCAGCGCTTTCCAGAAAGCTTTTCTGGAAGATCTTTGTGTGACAAAG	1137
Db	92999	TACCTTTGTCTCAGCGCTTTCCAGAAAGCTTTTCTGGAAGATCTTTGTGTGACAAAG	92940
QY	1138	CAACGAGCGCTGTACAGAACCACTCAGTATCTTCTGA	1176
Db	92939	CAACGAGCGCTGTACAGAACCACTCAGTATCTTCTGA	92901
RESULT 3			
AF358860			
LOCUS	AF358860	1593 bp	linear ROD 02-SEP-2001
DEFINITION	Rattus norvegicus histamine H4 receptor mRNA, complete cds.		
ACCESSION	AF358860		
VERSION	AF358860.1	GI:15420536	
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (bases 1 to 1593)		
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.		
TITLE	Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1593)		
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA		
FEATURES	Location/Qualifiers		
source	1. 1593		
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	/mol_type="mRNA"		
	/strain="Sprague-Dawley"		
	/db_xref="taxon:10116"		
	36..1211		
	/note="G-protein-coupled receptor"		
	/codon_start=1		
	/product="histamine H4 receptor"		
	/protein_id="AAK97381.1"		
	/db_xref="GI:15420537"		
	/translation="MSESNGTDVPLTAQVPLAFMLSLAFATIGNAVVILAFVADR		
CDS			

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 IATSRGCHSARTGLACTSLPGLKEPAASHSPSPGKSSLLVSLRTHMSGSLIAF
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ORIGIN

Query Match 5.7%; Score 67; DB 10; Length 1593;
 Best Local Similarity 100.0%; Pred. No. 4e-24; 0; Indels 0; Gaps 0;
 Matches 67; Conservative 0; Mismatches 0

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QY 290 TGTGCAC 296
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Db 325 TGTGCAC 331
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RESULT 4

AC118386/c

LOCUS

DEFINITION

AC118386

Accession

Version

Keywords

Source

Organism

REFERENCE

Authors

1 (bases 1 to 236694)

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyaibebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunarathne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,

Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuhera, L., Louised, H., Lozada, R. J., Lu, X., Ma, J.,

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,

Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwaokelemeh, O., Okwuon, G., Olarnpungsoo, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L.,

Puazo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,

Relly, B., Reilly, N., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,

Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstein, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 236694)

Worley, K. C.

Direct Submission

Submitted (17-APR-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 236694)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23812823.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature

table.

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GUEK

Center clone name: CH230-397N16

Summary Statistics

Assembly program: Phrap, version 0.990329

Consensus quality: 175902 bases at least Q40

Consensus quality: 179521 bases at least Q30

Consensus quality: 181489 bases at least Q20

Estimated insert size: 182948; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 3 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 217900: contig of 217900 bp in length

217901 218000: gap of unknown length

218001 234816: contig of 16816 bp in length

234817 234917: gap of unknown length

234917 236694: contig of 1778 bp in length.

Location/Qualifiers

1. 236694

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

FEATURES

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103725..105993
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120992..122993
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complement(209467..210237)
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clone_end:Sp6
site:
end sequence:BZ179483"
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216516..217900
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 TGTTAAGTGAATTTGGAAGTGAATCTGCATGTTTGGCTCATTAAGTACTATCTTT 289
Db 190285 TGTTAAGTGAATTTGGAAGTGAATCTGCATGTTTGGCTCATTAAGTACTATCTTT 190226

QY 290 TGTGCAC 296
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Db 190225 TGTGCAC 190219

RESULT 5
AB053300
LOCUS AB053300 1291 bp mRNA linear MAM 21-MAY-2002
DEFINITION Sus scrofa mRNA for histamine H4 receptor, complete cds.
ACCESSION AB053300
VERSION AB053300.1 GI:18147216
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
Oda,T., Matsumoto,S., Masuho,Y., Takasaki,J., Matsumoto,M.,
Kamohara,M., Saito,T., Ohishi,T., Soga,T., Hiyama,H., Matsushime,H.
and Furuichi,K.
cDNA cloning and characterization of porcine histamine H4 receptor
Biochim. Biophys. Acta 1575 (1-3), 135-138 (2002)
PUBMED 12020829
REFERENCE 2 (bases 1 to 1291)
Matsumoto,S., Oda,T. and Saito,Y.
Direct Submission
Submitted (08-JAN-2001) Shunichiro Matsumoto, Yamanouchi
Pharmaceutical Co., Ltd., Institute for Drug Discovery Research; 21
Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan
(E-mail:matsumot@yamanouchi.co.jp, Tel:81-298-54-1610,
Fax:81-298-52-5444)
FEATURES
Location/Qualifiers
source 1..1291
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CDS

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ORIGIN
Query Match 2.4%; Score 28; DB 4; Length 1291;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 AAACCTTAGACATCGAAGTAATATTTT 159
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Db 201 AAACCTTAGACATCGAAGTAATATTTT 228
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RESULT 6
AF358858
LOCUS AF358858 1451 bp mRNA linear ROD 02-SEP-2001
DEFINITION Cavia porcellus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358858
VERSION AF358858.1 GI:15420532
KEYWORDS
SOURCE Cavia porcellus (domestic guinea pig)
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 1451)
Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
REFERENCE 2 (bases 1 to 1451)
Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
FEATURES
Location/Qualifiers
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101..1270
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TECEPGFLKWEYLAITLFFFLAPVLAIVFNLYTYMSLWKRHLSCQSGCLSHVLPDS
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GFLSHSDSLALQOHEHIEFLFARKLAKSLAILLAICWAPYSLLTITRSVPTNP
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Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 TTTTGGCTCATTACTGACTATCTTT 290
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Db 362 TTTTGGCTCATTACTGACTATCTTT 387
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RESULT 7
AX775381
LOCUS AX775381 223 bp DNA linear PAT 09-JUL-2003

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DEFINITION Sequence 697 from Patent WO03038129.
ACCESSION AX775381
VERSION AX775381.1 GI:32486897
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kaponi,M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 697 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
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Query Match 1.9%; Score 22; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 966 TCTGTTCACAATTGTCCTTTCA 987
Db 197 TCTGTTCACAATTGTCCTTTCA 218
RESULT 8
BV056167 849 bp DNA linear STS 31-MAY-2003
LOCUS S212P6390FD12.TO CZECHII/El Mus musculus STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV056167
VERSION BV056167.1 GI:31171962
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Lander,E.S., Kulkobas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C.,
Wade,C.M., Lindblad-Toh,K. and Daly,M.J.
TITLE The mosaic structure of variation in the laboratory mouse genome
JOURNAL Nature 420 (6915), 574-578 (2002)
MEDLINE 22354684
COMMENT 12466852
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 849
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGSv3 C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated
as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 558 GCTTCTGTCATCTCTGTGGCT 579
Db 266 GCTTCTGTCATCTCTGTGGCT 287
RESULT 9
AR142850 1173 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 1 from patent US 6204017.
DEFINITION AR142850
ACCESSION AR142850
VERSION AR142850.1 GI:15104136
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P., and Wang,S.
TITLE Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..1173
/organism="unknown"
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Query Match 1.9%; Score 22; DB 6; Length 1173;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 966 TCTGTTCACAANTGTCCTTTCA 987
Db 960 TCTGTTCACAANTGTCCTTTCA 981
RESULT 10
AR391860 1173 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 1 from patent US 6613533.
DEFINITION AR391860
ACCESSION AR391860
VERSION AR391860.1 GI:40115588
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P., and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 966 TCTGTTCACAANTGTCCTTTCA 987
Db 960 TCTGTTCACAANTGTCCTTTCA 981

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RESULT 11
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LOCUS AX109119 1173 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0125432.
ACCESSION AX109119
VERSION AX109119.1 GI:13924093
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
Umland, S. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN
Query Match 1.9%; Score 22; DB 6; Length 1173;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCCAAATTGCTCTTTCA 987
|||||
Db 960 TCTGTTCCAAATTGCTCTTTCA 981

RESULT 12
AX139113
LOCUS AX139113 1173 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION AX139113
VERSION AX139113.1 GI:14274791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Peter, B. and O'Reilly, M.A.
TITLE G-protein coupled receptor-like polypeptide
JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.9%; Score 22; DB 6; Length 1173;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCCAAATTGCTCTTTCA 987
|||||
Db 960 TCTGTTCCAAATTGCTCTTTCA 981

RESULT 13
AX301763
LOCUS AX301763 1173 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 1 from Patent WO0185786.
ACCESSION AX301763
VERSION AX301763.1 GI:17382844
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
TITLE Human histamine h 42 receptor
JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;
American Home Products Corporation (US)
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCCAAATTGCTCTTTCA 987
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Db 960 TCTGTTCCAAATTGCTCTTTCA 981

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LOCUS BD015847 1173 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:22556984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
(bases 1 to 1173)
Peter, B. and Olayee, M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PFIZER INC
COMMENT OS Homo sapiens (human)
PN JP 2001211889-A/1
PD 07-AUG-2001
PR 27-OCT-2000 JP 2000329359
PF 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI
BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
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PC C07K14/00,
PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/10,
PC C12P21/02, C12Q1/02, G01N33/15, G01N33/50, G01N33/53//C12P21/08,
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PC A61K37/02, C12N5/00
CC Novel polypeptide
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

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DEFINITION Homo sapiens histamine H4 receptor mRNA, complete cds.
ACCESSION AF307973
VERSION AF307973.1 GI:11141732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Jones,P.G., Wu,S. and Betty,M.
TITLE Cloning of a novel histamine receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Jones,P.G., Wu,S. and Betty,M.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,
Princeton, NJ 08543, USA
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGTCCTTTCA 987
|||||
Db 960 TCTGTTCAACAATTGTCCTTTCA 981

Search completed: October 1, 2004, 17:38:46
Job time : 4885 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 13:52:44 ; Search time 857 Seconds
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5829.499 Million cell updates/sec

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Scoring table: OLIGO NUC

Searched: 3373863 seqs, 2124099041 residues

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Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	67	5.7	1176	6 AAI70982	Aai70982 Rat hista
3	30	2.6	30	6 AAI70992	Aai70992 Mouse his
4	29	2.5	29	6 AAI70991	Aai70991 Mouse his
5	26	2.2	1170	6 AAI70983	Aai70983 Guinea pi
6	23	2.0	39	6 AAI70993	Aai70993 Mouse his
7	22	1.9	223	9 ADE85481	Ade85481 Farnesyl
8	22	1.9	540	6 AAS98150	Aas98150 Human DNA
9	22	1.9	1103	8 AAD55123	Aad55123 Human H4
10	22	1.9	1166	8 AAD55124	Aad55124 Human H4
11	22	1.9	1170	8 AAD55126	Aad55126 Human H4
12	22	1.9	1173	3 AAA46023	Aaa46023 Human G p
13	22	1.9	1173	3 AAD01124	Aad01124 Human orp
14	22	1.9	1173	4 AAF83203	Aaf83203 Human GPC
15	22	1.9	1173	5 AAH24007	Aah24007 Human G p
16	22	1.9	1173	6 ABZ80663	Abz80663 Human his
17	22	1.9	1173	6 ABQ78739	Abq78739 Nucleotid
18	22	1.9	1173	6 AAI70980	Aai70980 Human his
19	22	1.9	1173	6 AAI67750	Aai67750 Human his
20	22	1.9	1173	7 ABS57063	Abs57063 Human cdn
21	22	1.9	1173	7 ACA93262	Aca93262 Human cdn
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23	22	1.9	1265	6 AAS98078	Aas98078 Human DNA

24	22	1.9	1265	8 AAD55125	Aad55125 Human H4
25	22	1.9	1266	6 ABK12959	Abk12959 DNA seque
26	22	1.9	1300	6 ABA02496	Aba02496 Human G p
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28	22	1.9	3689	7 ABZ42573	Abz42573 Human his
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30	21	1.8	867	2 AAT09949	Aat09949 High-affi
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32	21	1.8	220895	6 ABK84798	Abk84798 Human cdn
33	20	1.7	348	4 AAI80580	Aai80580 Human pol
34	20	1.7	536	4 AAS42963	Aas42963 DNA encod
35	20	1.7	693	7 ACA56900	Aca56900 Human cdn
36	20	1.7	693	7 ACA56899	Aca56899 Human cdn
37	20	1.7	867	4 AAF25245	Aaf25245 Nucleotid
38	20	1.7	1053	2 AAX05747	Aax05747 Human mel
39	20	1.7	1085	2 AAT09950	Aat09950 High-affi
40	20	1.7	1085	7 ACA56837	Aca56837 Human sig
41	20	1.7	1149	2 AAT09948	Aat09948 High-affi
42	20	1.7	1326	6 AAD37667	Aad37667 Human G-p
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ALIGNMENTS

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AC AAI70981;
XX
DT 18-MAR-2002 (first entry)
XX
DE Mouse histamine H4 receptor cDNA.
XX
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
XX
OS Mus musculus.
XX
FN WO200192485-A1.
XX
PD 06-DEC-2001.
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T, Liu C;
XX
DR WPI; 2002-114339/15.
DR P-ESDB; AAMS0565.
XX
New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
PS Claim 4; Fig 5A; 92pp; English.
XX
The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The cDNA was isolated from a mouse spleen cDNA library. It shows 72.8% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAMS0564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of

CC diseases where it is beneficial to elevate mammalian histamine H4
CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the mammalian histamine H4 receptor. Such modulators may be
CC useful for diagnosing, treating or preventing asthma, allergy,
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
CC disorders of the neuroendocrine system, stress and spasticity
XX
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Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TTAATGCTCTTCAATTCGCCCTTGTCTATAATGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120

QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTCTTAAATTTGGCTATTCT 180
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTCTTAAATTTGGCTATTCT 180

QY 181 GACTTCCTGTGGGTTGATTTCATTCCTCTGTACATCCCTCAGTGTGTTAACTGG 240
Db 181 GACTTCCTGTGGGTTGATTTCATTCCTCTGTACATCCCTCAGTGTGTTAACTGG 240

QY 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
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QY 301 TCTGTCTACAAATATGTCTCATTAGCTACGATCGATACCAGTCAAGTTCAAATGCTGTG 360
Db 301 TCTGTCTACAAATATGTCTCATTAGCTACGATCGATACCAGTCAAGTTCAAATGCTGTG 360

QY 361 TCTTATAGGCTCAACACATCTGCATGCAATGATGTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGGCTCAACACATCTGCATGCAATGATGTTGCTCAAAATGGTGGCTGTTGG 420

QY 421 ATACTGGCTTCTTGTGTAATGTCGCGATGATTTCTGGCTTCAGATTCTTGGAAAGAACAGC 480
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QY 1081 CTTTGTGTGTCACAGGCTTTCCAGAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140
Db 1081 CTTTGTGTGTCACAGGCTTTCCAGAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140

QY 1141 CCAGCGCTGTACAGAACCCAGTCAGTATCTTTTGA 1176
Db 1141 CCAGCGCTGTACAGAACCCAGTCAGTATCTTTTGA 1176

RESULT 2

AAI70982
ID AAI70982 standard; cDNA; 1176 BP.
XX
AC AAI70982;
XX
DT 18-MAR-2002 (first entry)
XX
DE Rat histamine H4 receptor cDNA.
XX
KW Histamine H4 receptor; rat; antiallergic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
XX
OS Rattus rattus.
XX
PN WO200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US0005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T, Liu C;
XX
PI WPI; 2002-114339/15.
XX
DR P-PSDB; AAM50566.
XX
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
PS Claim 4; Fig 5C; 92pp; English.
XX

CC The present sequence is that of a cDNA clone encoding a rat histamine
CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA
CC library. It shows 72.5% homology to the human H4 receptor coding region.
CC The invention provides mammalian (human, mouse, rat and guinea pig)
CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC recombinant host cells that produce active recombinant protein. The
CC pharmacology of known histamine ligands is demonstrated. Mammalian
CC histamine H4 receptor may be used in gene therapy for the treatment of
CC diseases where it is beneficial to elevate mammalian histamine H4
CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the mammalian histamine H4 receptor. Such modulators may be
CC useful for diagnosing, treating or preventing asthma, allergy,
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin

CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
 CC disorders of the neuroendocrine system, stress and spasticity
 XX Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;
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 Best Local Similarity 100.0%; Pred. No. 9.2e-23;
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QY 290 TGTGCAC 296
 DB 290 TGTGCAC 296

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 AAI70992
 ID AAI70992 standard; DNA; 30 BP.
 AC AAI70992;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE Mouse histamine H4 receptor gene specific primer P2.
 XX
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
 KW diagnosis; gene therapy; PCR primer; RACE; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200192485-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 22-FEB-2001; 2001WO-US005914.
 XX
 PR 31-MAY-2000; 2000US-0208260P.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 PI Lovenberg T, Liu C;
 XX
 DR WPI; 2002-114339/15.
 XX
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.
 XX
 PS Example 10; Page 48; 92pp; English.
 XX
 CC The present sequence is that of mouse histamine H4 receptor gene specific
 CC primer P2, which was used with an adaptor primer (see AAI70990) in a 3',
 CC RACE amplification of mouse spleen cDNA. Full-length cDNA (see AAI70981)
 CC encoding mouse H4 (see AAM50565) was subsequently obtained. The invention
 CC provides mammalian histamine H4 receptor nucleic acid molecules and
 CC polypeptides. The nucleic acids have been expressed in recombinant host
 CC cells that produce active recombinant protein. Mammalian histamine H4
 CC receptor may be used in gene therapy for the treatment of diseases where
 CC it is beneficial to elevate mammalian histamine H4 receptor activity.
 CC Recombinant H4 receptor protein can be used to identify modulators of
 CC activity for use in the treatment of asthma, allergy, inflammation,
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
 CC the neuroendocrine system, stress and spasticity
 XX
 SQ Sequence 30 BP; 8 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 2.6%; Score 30; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 TGCATCTCGTCACTCAGAAAGTCTCGAAG 770
 DB 1 TGCATCTCGTCACTCAGAAAGTCTCGAAG 30

RESULT 4
 AAI70991/C
 ID AAI70991 standard; DNA; 29 BP.
 XX
 AC AAI70991;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE Mouse histamine H4 receptor gene specific primer P1.
 XX
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
 KW diagnosis; gene therapy; PCR primer; RACE; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200192485-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 22-FEB-2001; 2001WO-US005914.
 XX
 PR 31-MAY-2000; 2000US-0208260P.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 PI Lovenberg T, Liu C;
 XX
 DR WPI; 2002-114339/15.
 XX
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.
 XX
 PS Example 10; Page 48; 92pp; English.
 XX
 CC The present sequence is that of mouse histamine H4 receptor gene specific
 CC primer P1, which was used with an adaptor primer (see AAI70990) in a 5',
 CC RACE amplification of mouse spleen cDNA. Full-length cDNA (see AAI70981)
 CC encoding mouse H4 (see AAM50565) was subsequently obtained. The invention
 CC provides mammalian histamine H4 receptor nucleic acid molecules and
 CC polypeptides. The nucleic acids have been expressed in recombinant host
 CC cells that produce active recombinant protein. Mammalian histamine H4
 CC receptor may be used in gene therapy for the treatment of diseases where
 CC it is beneficial to elevate mammalian histamine H4 receptor activity.
 CC Recombinant H4 receptor protein can be used to identify modulators of
 CC activity for use in the treatment of asthma, allergy, inflammation,
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
 CC the neuroendocrine system, stress and spasticity
 XX
 SQ Sequence 29 BP; 9 A; 10 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.5%; Score 29; DB 6; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GACTGTGAGCTGCGCTTTTGTACAGAGTG 521
 DB 29 GACTGTGAGCTGCGCTTTTGTACAGAGTG 1

RESULT 5
 AAI70983
 ID AAI70983 standard; cDNA; 1170 BP.
 XX

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AC AAI70983;
XX
XX 18-MAR-2002 (first entry)
XX
DE Guinea pig histamine H4 receptor cDNA.
XX
XX Histamine H4 receptor; guinea pig; antiasthmatic; antiallergenic;
KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
XX
OS Cavia porcellus.
XX
XX WO200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
XX
XX P-PSDB; AAM50567.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Claim 4; Fig 6B; 92pp; English.
XX
XX The present sequence is that of a cDNA clone encoding guinea pig
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. It shows 75.6% homology to the human H4 receptor
CC coding region. The invention provides mammalian (human, mouse, rat and
CC guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-
CC 83) and polypeptides (see AAM50564-67). The nucleic acids have been
CC expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the mammalian histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
XX Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;

Query Match 2.2%; Score 26; DB 6; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 TTTGGCTCATTACTGACTATCTTTT 290
DB 262 TTTGGCTCATTACTGACTATCTTTT 287

RESULT 6
AAI70993
ID AAI70993 standard; DNA; 39 BP.
AC AAI70993;
XX
XX 18-MAR-2002 (first entry)
XX
XX Mouse histamine H4 receptor cDNA forward PCR primer.
DE
XX Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
XX

```

```

KW diagnosis; gene therapy; PCR primer; ss.
XX
XX Mus musculus.
XX
XX WO200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Example 10; Page 49; 92pp; English.
XX
XX The present sequence is that of the forward primer used, with the reverse
CC primer given in AAI70994, in the PCR amplification of mouse spleen cDNA.
CC The coding region (see AAI70981) of mouse histamine H4 receptor cDNA was
CC obtained. The PCR product was cloned into mammalian expression vector
CC pcNeo. The invention provides mammalian histamine H4 receptor nucleic
CC acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The
CC nucleic acids have been expressed in recombinant host cells that produce
CC active recombinant protein. Mammalian histamine H4 receptor may be used
CC in gene therapy for the treatment of diseases where it is beneficial to
CC elevate mammalian histamine H4 receptor activity. Recombinant H4 receptor
CC protein can be used to identify modulators of activity for use in the
CC treatment of asthma, allergy, inflammation, cardiovascular and
CC cerebrovascular disorders, non-insulin dependent diabetes mellitus,
CC hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine
CC system, stress and spasticity
XX
XX Sequence 39 BP; 11 A; 10 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 23; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAGTCTAACAGTACTGG 23
DB 17 ATGTCGAGTCTAACAGTACTGG 39

RESULT 7
ADE85481
ID ADE85481 standard; DNA; 223 BP.
XX
XX ADE85481;
XX
XX 29-JAN-2004 (first entry)
XX
XX
DE Farnesyl transferase inhibitor modulated leukemia associated gene #700.
KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW quinolinone; leukemia; cancer.
XX
XX Homo sapiens.
XX
XX WO2003038129-A2.
XX
XX 08-MAY-2003.
XX
XX 30-OCT-2002; 2002WO-US034784.
XX
XX 30-OCT-2001; 2001US-0338997P.

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PR 30-OCT-2001; 2001US-0340081P.
PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX PA
XX Raponi M;
XX WI; 2003-513497/48.
XX
XX Determining whether a patient will respond to treatment with a farnesyl
XX transferase inhibitor, by analyzing the expression of gene that is
XX differentially modulated in the presence of the inhibitor.
XX
XX Disclosure; SEQ ID NO 700; 346pp; English.
XX
XX The invention relates to a method of determining whether a patient will
XX respond to treatment with a farnesyl transferase inhibitor (FTI), by
XX analyzing the expression of gene that is differentially modulated in the
XX presence of an FTI. The method is useful for determining whether a
XX patient will respond to treatment with a FTI such as (B)-6-[amino(4-
XX chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
XX methyl-2-(1H)quinoline, monitoring the therapy of a patient, treating a
XX patient with leukemia with FTI if the analysis indicates that the patient
XX will respond. This sequence corresponds to a gene whose expression may be
XX modulated in the presence of FTI.
XX
XX Sequence 223 BP; 57 A; 49 C; 43 G; 73 T; 0 U; 1 Other;
XX
XX
XX Query Match 1.9%; Score 22; DB 9; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 966 TCTGTTTCACAAATTGTCCTTTCA 987
XX |||||||||||||||||||
XX Db 197 TCTGTTTCACAAATTGTCCTTTCA 218
XX
XX
XX RESULT 8
XX AAS98150/C
XX ID AAS98150 standard; DNA; 540 BP.
XX
XX AC AAS98150;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human DNA for potential G protein-coupled receptor #107.
XX
XX Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
XX Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
XX atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
XX chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
XX depression; epilepsy; macular degeneration; lymphoma; melanoma;
XX multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
XX psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
XX tuberculosis; cognition disorder; memory disorder; anorexia;
XX hormonal release disorder; cardiovascular activity disorder;
XX pain perception disorder; obesity; diabetes; obesity; diabetes;
XX hyperlipidaemia; stroke; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200185791-A1.
XX
XX 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-US015332.
XX
XX 11-MAY-2000; 2000US-0203217P.
XX
XX 18-MAY-2000; 2000US-0205945P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;
XX WI; 2002-066595/09.
XX
XX Novel G protein-coupled receptor polypeptides including galanin receptor
XX polypeptides useful for identifying modulators that are useful for
XX treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
XX stroke.
XX
XX Claim 2; Page 106; 144pp; English.
XX
XX The invention relates to an isolated polypeptide encoded by a nucleic
XX acid molecule that is at least 80% identical to the G protein-coupled
XX (GPCR) polynucleotides included in the specification. Also included are
XX probes based on the GPCR sequences (including antisense probes), a host
XX cell comprising an expression vector comprising the GPCR sequence,
XX antibodies raised against the polypeptides, and methods of identifying
XX modulators of the polypeptides. The polypeptides are useful for
XX identifying modulator compounds which function as modulators, activators,
XX repressors, agonists or antagonists of the novel GPCR polypeptides
XX including the GAL4 polypeptide. The antibodies and nucleic acid probes as
XX described above can be used to detect the presence of the polypeptides
XX and nucleic acids and are used to diagnose a variety of diseases or
XX disorders in which GPCRs are involved e.g., Alzheimer's disease,
XX amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell
XX carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic
XX obstructive pulmonary disease, Crohn's disease, depression, epilepsy,
XX macular degeneration, lymphoma, melanoma, multiple sclerosis,
XX osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid
XX arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other
XX diseases listed in the specification. The probes and antibodies are also
XX useful for diagnosing cognition and memory disorders, anorexia, hormonal
XX release disorders, cardiovascular activity disorders, pain perception
XX disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds
XX that decrease or increase the expression of galanin receptor (GAL4) can
XX be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR
XX nucleic acid is useful for treating the above mentioned disorders by gene
XX therapy techniques. The present sequence is a novel GPCR polynucleotide
XX of the invention
XX
XX Sequence 540 BP; 173 A; 107 C; 119 G; 138 T; 0 U; 3 Other;
XX
XX Query Match 1.9%; Score 22; DB 6; Length 540;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 966 TCTGTTTCACAAATTGTCCTTTCA 987
XX |||||||||||||||||||
XX Db 173 TCTGTTTCACAAATTGTCCTTTCA 152
XX
XX
XX RESULT 9
XX AAD55123
XX ID AAD55123 standard; DNA; 1103 BP.
XX
XX AC AAD55123;
XX
XX 07-AUG-2003 (first entry)
XX
XX Human H4 receptor splice variant (H4b) DNA.
XX
XX Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
XX atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
XX chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
XX rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
XX asthma; receptor; variant; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 55..1065
XX /*tag= a
XX /product= "Human H4b protein"
XX

```

```

XX WO2003020907-A2.
XX
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027891.
XX PF
XX 31-AUG-2001; 2001US-0316762P.
XX PR
XX 13-NOV-2001; 2001US-0332697P.
XX
XX (MERI ) MERCK & CO INC.
XX PA
XX Gallagher MJ, Yates SL;
XX PI
XX WPI: 2003-290186/28.
XX DR
XX P-PSDB; AAE36414.
XX
XX Novel splice variants of human H4 histamine receptor, H4b and H4c, useful
XX for identifying agonists or antagonists of the receptor which are useful
XX for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
XX
XX Claim 5; Page 44-46; 31pp; English.
XX
XX The invention relates to splice variants of human H4 histamine receptor,
XX H4b and H4c. The invention is useful for identifying an agonist,
XX antagonist or inverse agonist of a mammalian histamine receptor. The
XX agonist, antagonist or inverse agonist of H4b and H4c is useful for
XX treating inflammation, asthma, allergy, atopic dermatitis, stroke,
XX myocardial infarction, migraine, chronic obstructive pulmonary disease
XX (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
XX disease, or psoriasis. The present sequence is human H4b DNA
XX
XX Sequence 1103 BP; 275 A; 226 C; 217 G; 385 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 22; DB 8; Length 1103;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 966 TCTGTTCACAATTGTCCTTTCA 987
XX |||||
XX Db 852 TCTGTTCACAATTGTCCTTTCA 873
XX
XX RESULT 10
XX AAD55124
XX ID AAD55124 standard; DNA; 1166 BP.
XX
XX AC AAD55124;
XX
XX DT 07-AUG-2003 (first entry)
XX
XX DE Human H4 receptor splice variant (H4c) DNA.
XX
XX KW Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
XX atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
XX chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
XX rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
XX asthma; receptor; variant; gene; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 55..1128
XX /*tag= a
XX /product= "Human H4c protein"
XX
XX WO2003020907-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027891.
XX PF
XX 31-AUG-2001; 2001US-0316762P.
XX PR
XX 13-NOV-2001; 2001US-0332697P.
XX
XX (MERI ) MERCK & CO INC.
XX PA
XX Gallagher MJ, Yates SL;
XX PI
XX
XX

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PR 13-NOV-2001; 2001US-0332697P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Gallagher MJ, Yates SL;
XX PI
XX WPI: 2003-290186/28.
XX DR
XX P-PSDB; AAE36415.
XX
XX Novel splice variants of human H4 histamine receptor, H4b and H4c, useful
XX for identifying agonists or antagonists of the receptor which are useful
XX for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
XX
XX Claim 17; Page 48-49; 31pp; English.
XX
XX The invention relates to splice variants of human H4 histamine receptor,
XX H4b and H4c. The invention is useful for identifying an agonist,
XX antagonist or inverse agonist of a mammalian histamine receptor. The
XX agonist, antagonist or inverse agonist of H4b and H4c is useful for
XX treating inflammation, asthma, allergy, atopic dermatitis, stroke,
XX myocardial infarction, migraine, chronic obstructive pulmonary disease
XX (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
XX disease, or psoriasis. The present sequence is human H4c DNA
XX
XX Sequence 1166 BP; 294 A; 246 C; 218 G; 408 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 22; DB 8; Length 1166;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 966 TCTGTTCACAATTGTCCTTTCA 987
XX |||||
XX Db 915 TCTGTTCACAATTGTCCTTTCA 936
XX
XX RESULT 11
XX AAD55126
XX ID AAD55126 standard; DNA; 1170 BP.
XX
XX AC AAD55126;
XX
XX DT 07-AUG-2003 (first entry)
XX
XX DE Human H4 receptor wild-type DNA #2.
XX
XX KW Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
XX atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
XX chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
XX rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
XX asthma; receptor; gene; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1170
XX /*tag= a
XX /product= "Human H4 protein"
XX /note= "CDS does not include stop codon"
XX /partial
XX
XX WO2003020907-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027891.
XX PF
XX 31-AUG-2001; 2001US-0316762P.
XX PR
XX 13-NOV-2001; 2001US-0332697P.
XX
XX (MERI ) MERCK & CO INC.
XX PA
XX Gallagher MJ, Yates SL;
XX PI
XX

```

DR WPI; 2003-290186/28.
 DR P-PSDB; AAE36417.
 XX
 PT Novel splice variants of human H4 histamine receptor, H4b and H4c, useful
 PT for identifying agonists or antagonists of the receptor which are useful
 PT for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
 XX
 PS Disclosure; Page 56-58; 31pp; English.
 XX
 CC The invention relates to splice variants of human H4 histamine receptor,
 CC H4b and H4c. The invention is useful for identifying an agonist,
 CC antagonist or inverse agonist of a mammalian histamine receptor. The
 CC agonist, antagonist or inverse agonist of H4b and H4c is useful for
 CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,
 CC myocardial infarction, migraine, chronic obstructive pulmonary disease
 CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
 CC disease, or psoriasis. The present sequence is human H4 receptor DNA
 XX
 SQ Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;
 Query Match 1.9%; Score 22; DB 8; Length 1170;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 966 TCTGTTCAACAATGTCTTTCA 987
 Db 960 TCTGTTCAACAATGTCTTTCA 981
 RESULT 12
 AAA46023
 ID AAA46023 standard; cDNA; 1173 BP.
 XX
 AC AAA46023;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WC200022131-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US024065.
 XX
 PR 13-OCT-1998; 98US-00170496.
 PR 12-NOV-1998; 98US-0108029P.
 PR 20-NOV-1998; 98US-0109213P.
 PR 27-NOV-1998; 98US-0110060P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123944P.
 PR 12-MAR-1999; 99US-0123945P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123948P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 12-MAR-1999; 99US-0123951P.
 PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 28-MAY-1999; 99US-0137567P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 27-AUG-1999; 99US-0151114P.
 PR 03-SEP-1999; 99US-0152524P.
 PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156653P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157293P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 XX WPI; 2000-317986/27.
 DR P-PSDB; AAB02831.
 DR
 XX Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT inverse or partial agonists useful as therapeutic agents.
 XX
 PS Example 1; Page 88-89; 187pp; English.
 XX
 CC The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptors agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Query Match 1.9%; Score 22; DB 3; Length 1173;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 966 TCTGTTCAACAATGTCTTTCA 987
 Db 960 TCTGTTCAACAATGTCTTTCA 981
 RESULT 13
 AAD01124
 ID AAD01124 standard; cDNA; 1173 BP.
 XX
 AC AAD01124;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Human orphan G protein-coupled receptor hRUP7 cDNA.
 XX
 KW Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;
 KW transmembrane receptor; signal cascade; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1173
 FT /*tag= a
 FT /product= "hRUP7"
 FT /note= "Human orphan G protein-coupled receptor"
 XX
 PN WC200031258-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 13-OCT-1999; 99WO-US023687.
 XX
 PR 20-NOV-1998; 98US-0109213P.


```
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123946P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Liaw CW, Lin I;
XX
XX WPI; 2000-400068/34.
DR P-PSDB; AAY71297.
XX
PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for
PT use in the identification of G protein-coupled receptor agonists.
XX
PS Claim 25; Page 59; 102pp; English.
XX
CC The present sequence is a cDNA encoding hRUP7, an endogenous human orphan
CC G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned
CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
CC GPCR of the invention, like all GPCRs has seven transmembrane alpha
CC helices with an extracellular N-terminus and an intracellular C-terminus.
CC However, no endogenous ligands has yet been identified for the proteins
CC of the invention. The orphan GPCRs may be used in the identification of
CC their endogenous ligands, and to screen potential GPCR agonists and
CC antagonists for use as pharmaceutical agents. The proteins may also be
CC used in the study of GPCR-mediated signalling cascades, and to elucidate
CC their precise role in normal and diseased human conditions. Nucleic acid
CC encoding human orphan GPCRs may be used for tissue localisation in
CC expression analysis to provide information about their function in
CC healthy and pathological states
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 1.9%; Score 22; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 966 TCTGTTCAAAATGTCCTTTCA 987
DB 960 TCTGTTCAAAATGTCCTTTCA 981
RESULT 14
AAF83203
ID AAF83203 standard; cDNA; 1173 BP.
XX
AC AAF83203;
XX
DT 09-JUL-2001 (first entry)
XX
DE Human GPCR-like polypeptide, PFI-013 encoding cDNA.
XX
KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;
KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
osteopathic; neuroprotective; nootropic; dermatological; gynecological;
signal transduction; ss.
KW Homo sapiens.
XX
Key Location/Qualifiers
CDS 1..1173
FT /*tag= a
FT /product= "PFI-013"
XX
PN EP1096009-A1.
XX
XX 02-MAY-2001.
XX
XX 24-OCT-2000; 2000EP-00309364.
PR 29-OCT-1999; 99GB-00025641.
PR 20-APR-2000; 2000GB-00009973.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Peter B, O'reilly MA;
XX
XX WPI; 2001-309854/33.
DR P-PSDB; AAB62445.
XX
PT New G-protein coupled receptor-like polypeptide, polynucleotide for
PT screening drug candidates for treating diseases associated with signal
PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
PS Claim 1; Page 43; 66pp; English.
XX
CC This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
CC expressed by standard recombinant methodology. Antibodies and modulators
CC of PFI-013 are useful in the manufacture of a medicament for treating
CC allergic disorder, including extrinsic asthma, immunological disorders,
CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial
CC and other pulmonary disease, including chronic obstructive pulmonary
CC disease (COPD), infectious, inflammatory disease, such as inflammatory
CC bowel disease and neoplastic and myeloproliferative diseases. They are
CC also useful for treating obesity, diabetes, metabolic, neurological
CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual
CC medicine, inflammation, cancer, tissue repair, dermatology, photoaging,
CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
CC diseases, allergy and respiratory disease, sensory organ disorders, sleep
CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful
CC in the diagnosis and treatment of the above conditions and also for
CC screening drug candidates for the treatment of diseases associated with
CC signal transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 1.9%; Score 22; DB 4; Length 1173;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 966 TCTGTTCAAAATGTCCTTTCA 987
DB 960 TCTGTTCAAAATGTCCTTTCA 981
RESULT 15
AAH24007
ID AAH24007 standard; cDNA; 1173 BP.
XX
AC AAH24007;
XX
DT 10-AUG-2001 (first entry)
XX
```

DE Human G protein-coupled receptor AXOR35 cDNA.
XX
XX AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW manic depression; neurological disorder; depression; anxiety; schizophrenia;
KW severe mental retardation; dyslexia; Parkinson's disease;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..1173
FT CDS /*tag= a
FT /product= "Human AXOR35"
FT /note= "G protein-coupled receptor"
XX
XX WO200133221-A1.
XX
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX (SMK) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;
PI Michalovich D, Morrow DM, Zhu Y;
XX
XX WPI; 2001-316464/33.
XX P-PSDB; AAB73622.
XX
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
PT disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 2; Page 49-50; 54pp; English.
XX
XX The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC and nucleotides may be used to treat a wide variety of disorders
CC including bacterial, fungal, protozoal and viral infections, particularly
CC HIV-1 or HIV-2 infections; pain; cancer; benign prostatic hypertrophy;
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
CC urinary retention; acute heart failure; hypotension; hypertension; angina
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia, and severe mental
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
CC antibodies may be used in screening compounds for their ability to
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
CC particularly useful for treating asthma, and inhibiting or promoting the
CC function of lymphocytes, macrophages, eosinophils or neutrophils in
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also

CC useful for diagnosing or determining susceptibility of an individual to a
CC disease via the detection of abnormal levels of protein or mRNA, or via
CC the detection of mutations in the corresponding gene. AXOR35 proteins are
CC also useful for inducing an immunological response in a mammal against
CC the above diseases, and for antibody production. AXOR35 nucleotides are
CC also useful as diagnostic reagents, in chromosome localisation and tissue
CC expression studies, and for producing transgenic animals useful in drug
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
CC protein or fragments thereof, and are also useful for treating conditions
CC associated with the expression of the AXOR35 protein. The present
CC sequence represents cDNA encoding human AXOR35
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
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Query Match 1.9%; Score 22; DB 5; Length 1173;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 966 TCTGTTCACAAATTGTCCTTTCA 987
|||
DB 960 TCTGTTCACAAATTGTCCTTTCA 981
|||
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Job time : 862 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
5932.930 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atgtcggagcttaacagctac.....accagtcagtatcttcttga 1176

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/2/ina/PCRUS_COMB.seq.*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	1.9	1173	US-09-414-010-1	Sequence 1, Appli
2	22	1.9	1173	US-09-812-216-1	Sequence 1, Appli
3	21	1.8	867	US-08-466-103A-5	Sequence 5, Appli
4	20	1.7	1085	US-08-466-103A-11	Sequence 11, Appl
5	20	1.7	1085	US-09-016-434-1435	Sequence 1435, Ap
6	20	1.7	1149	US-08-466-103A-3	Sequence 3, Appli
7	19	1.6	453	US-09-134-000C-1014	Sequence 1014, Ap
8	19	1.6	5229	US-09-635-872A-16	Sequence 16, Appl
9	19	1.6	5229	US-09-636-077A-16	Sequence 16, Appl
10	19	1.6	5229	US-09-636-060C-16	Sequence 16, Appl
11	19	1.6	5229	US-09-986-552-16	Sequence 16, Appl
12	19	1.6	152331	US-09-128-155-16	Sequence 16, Appl
13	18	1.5	424	US-09-621-976-7975	Sequence 7975, Ap
14	18	1.5	536	US-08-341-568-1	Sequence 1, Appli
15	18	1.5	536	US-08-911-020-1	Sequence 1, Appli
16	18	1.5	2278	US-09-620-312D-1003	Sequence 1003, Ap
17	18	1.5	2278	US-09-148-545-78	Sequence 78, Appl
18	18	1.5	2278	US-09-148-545-131	Sequence 131, App
19	18	1.5	152331	US-09-128-155-16	Sequence 16, Appl
20	18	1.5	176373	US-09-128-155-17	Sequence 17, Appl
21	17	1.4	526	US-08-956-171E-516	Sequence 516, App
22	17	1.4	539	US-09-833-381-114	Sequence 114, App
23	17	1.4	675	US-09-621-976-2461	Sequence 2461, Ap
24	17	1.4	945	US-09-489-039A-2349	Sequence 2349, App
25	17	1.4	1368	US-09-540-236-405	Sequence 405, App
26	17	1.4	1503	US-09-254-465A-5	Sequence 5, Appli
27	17	1.4	1558	US-09-198-603C-24	Sequence 24, Appl

28	17	1.4	1590	4	US-09-369-247-14	Sequence 14, Appli
29	17	1.4	1620	4	US-09-554-080A-1	Sequence 1, Appli
30	17	1.4	1744	4	US-09-484-970B-83	Sequence 83, Appl
31	17	1.4	2088	4	US-09-489-039A-7167	Sequence 7167, Ap
32	17	1.4	2176	4	US-08-956-171E-445	Sequence 445, App
33	17	1.4	2181	4	US-09-254-465A-7	Sequence 7, Appli
34	17	1.4	2181	4	US-09-254-465A-11	Sequence 11, Appl
35	17	1.4	2565	4	US-09-023-655-1052	Sequence 1052, Ap
36	17	1.4	2861	4	US-09-016-434-1103	Sequence 1103, Ap
37	17	1.4	4746	2	US-08-819-288-2	Sequence 2, Appli
38	17	1.4	4746	4	US-09-400-348-2	Sequence 2, Appli
39	17	1.4	4747	1	US-08-261-822A-2	Sequence 2, Appli
40	17	1.4	4747	5	PCT-US95-07744A-2	Sequence 2, Appli
41	17	1.4	6042	1	US-08-261-822A-1	Sequence 1, Appli
42	17	1.4	6042	5	PCT-US95-07744A-1	Sequence 1, Appli
43	17	1.4	6172	2	US-08-819-288-1	Sequence 1, Appli
44	17	1.4	6172	4	US-09-400-348-1	Sequence 1, Appli
45	17	1.4	6387	1	US-07-721-775A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Query Match 1.9%; Score 22; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCACAATTGTCCTTCA 987
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Db 960 TCTGTTCACAATTGTCCTTCA 981

RESULT 2
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010

QY 939 TTTTGCCATTGCTGGCTCC 959
DB 552 TTTTGCCATTGCTGGCTCC 572

RESULT 4
US-08-466-103A-11
; Sequence 11, Application US/08466103A
; Patent No. 5856124
; GENERAL INFORMATION:
; APPLICANT: Reppert, Steven M.
; APPLICANT: Ebisawa, Takashi
; TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/08/466.103A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/319,887
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/261,857
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/250002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 33...1082
; OTHER INFORMATION:
US-08-466-103A-11

Query Match 1.7%; Score 20; DB 2; Length 1085;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 940 TTTTGCCATTGCTGGCTCC 959
DB 771 TTTTGCCATTGCTGGCTCC 790

RESULT 5
US-09-016-434-1435
; Sequence 1435, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young

QY 966 TCTGTTCAATTCCTTTCA 987
DB 960 TCTGTTCAATTCCTTTCA 981

US-09-812-216-1

US-08-466-103A-5
; Sequence 5, Application US/08466103A
; Patent No. 5856124
; GENERAL INFORMATION:
; APPLICANT: Reppert, Steven M.
; APPLICANT: Ebisawa, Takashi
; TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/08/466.103A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/319,887
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/261,857
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/250002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 867 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...864
; OTHER INFORMATION:
US-08-466-103A-5

Query Match 1.8%; Score 21; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Issued 1/5/99

APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1435:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9602129
US-09-016-434-1435

Query Match 1.7%; Score 20; DB 4; Length 1085;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 940 TTGGCATTGTGGGCTCC 959
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Db 771 TTGGCATTGTGGGCTCC 790

RESULT 6
US-08-466-103A-3
Sequence 3, Application US/08466103A
Patent No. 5856124
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,103A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 49...1146
OTHER INFORMATION:
US-08-466-103A-3

Query Match 1.7%; Score 20; DB 2; Length 1149;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 940 TTGGCATTGTGGGCTCC 959
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Db 835 TTGGCATTGTGGGCTCC 854

RESULT 7
US-09-134-000C-1014/c
Sequence 1014, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1014
LENGTH: 453
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-1014

Query Match 1.6%; Score 19; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AATTATTTTCTTAATT 169
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Db 282 AATTATTTTCTTAATT 264

RESULT 8
US-09-635-872A-16/c
Sequence 16, Application US/09635872A
Patent No. 6534300

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; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 195613US0
; CURRENT APPLICATION NUMBER: US/09/635,872A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-635-872A-16

Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 9
US-09-636-077A-16/c
; Sequence 16, Application US/09636077A
; Patent No. 6537785
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; FILE REFERENCE: 195612US0
; CURRENT APPLICATION NUMBER: US/09/636,077A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-636-077A-16

Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 10
US-09-636-060C-16/c
; Sequence 16, Application US/09636060C
; Patent No. 6642038
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: GLCNAC PHOSPHOTRANSFERASE OF THE LYSOSOMAL TARGETING PATHWAY
; FILE REFERENCE: 210119US0CONT
; CURRENT APPLICATION NUMBER: US/09/636,060C
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-636-060C-16
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Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 11
US-09-986-552-16/c
; Sequence 16, Application US/09986552
; Patent No. 6670165
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 215089US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-986-552-16

Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 12
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -- (152331)
; OTHER INFORMATION: n = A,T,C or G
; US-09-128-155-16

Query Match      1.6%; Score 19; DB 3; Length 152331;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      911 CCAGGTCACTGGCCATCCT 929
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Db 135343 CCAGGTCACTGGCCATCCT 135325
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RESULT 13

US-09-621-976-7975
; Sequence 7975, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7975
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-7975

Query Match 1.5%; Score 18; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 CTCCTGGAAATTCGTCT 561

Db 40 CTCCTGGAAATTCGTCT 57

RESULT 14

US-08-341-568-1
; Sequence 1, Application US/08341568
; Patent No. 5661021
; GENERAL INFORMATION:
; APPLICANT: Buchert, Johanna
; APPLICANT: Siika-aho, Matti
; APPLICANT: Viikari, Liisa
; APPLICANT: Penttila, Merja
; APPLICANT: Saloheimo, Anu
; APPLICANT: Marjatta, Rannu
; TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
; TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching lig
; TITLE OF INVENTION: pulps
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: PO Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: US
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/341,568
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr, Gerald M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 365-262P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Trichoderma reesei
; STRAIN: QM9414
US-08-341-568-1

; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma reesei
; STRAIN: QM9414
US-08-341-568-1

Query Match 1.5%; Score 18; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 CTGGAGCCTGTGGAAGCG 617

Db 128 CTGGAGCCTGTGGAAGCG 145

RESULT 15

US-08-911-020-1
; Sequence 1, Application US/08911020
; Patent No. 5854047
; GENERAL INFORMATION:
; APPLICANT: Buchert, Johanna
; APPLICANT: Siika-aho, Matti
; APPLICANT: Viikari, Liisa
; APPLICANT: Penttila, Merja
; APPLICANT: Saloheimo, Anu
; APPLICANT: Marjatta, Rannu
; TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
; TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching
; TITLE OF INVENTION: lignocellulosic pulps
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: PO Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: US
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,020
; FILING DATE: 13-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/341,568
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr, Gerald M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 365-262P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; MOLECULE TYPE: cDNA
; ORGANISM: Trichoderma reesei
; STRAIN: QM9414
US-08-911-020-1

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Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 CTGGAGCCTGTGGAGCG 617
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Db 128 CTGGAGCCTGTGGAGCG 145

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Job time : 113 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783454 residues

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Minimum DB seq length: 0

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	1.9	223	17	US-10-283-975A-697
2	22	1.9	1173	9	Sequence 697, Appl
3	22	1.9	1173	9	Sequence 1, Appli
4	22	1.9	1173	9	Sequence 1, Appli
5	22	1.9	1173	13	US-10-349-253A-1
6	22	1.9	1173	13	US-09-875-076-13
7	22	1.9	1173	13	US-08-876-252-13
8	22	1.9	1173	14	US-10-052-193-1
9	22	1.9	1173	15	US-10-290-078-26
10	22	1.9	1173	15	US-10-272-983-13
11	22	1.9	1173	15	US-10-354-769-1
12	22	1.9	1173	15	US-10-393-807-13
13	22	1.9	1173	16	US-10-417-820A-13
14	22	1.9	1173	17	US-10-723-955-13
15	22	1.9	1173	17	US-10-737-619-1

15	22	1.9	1173	17	US-10-782-596-13	Sequence 13, Appl
16	22	1.9	1265	15	US-10-290-078-25	Sequence 25, Appl
17	22	1.9	1266	10	US-09-891-138A-5	Sequence 5, Appli
18	22	1.9	1300	10	US-09-852-165-1	Sequence 1, Appli
19	22	1.9	1300	17	US-10-696-673-1	Sequence 1, Appli
20	22	1.9	3689	15	US-10-225-567A-628	Sequence 628, App
21	21	1.8	633	13	US-10-027-632-274218	Sequence 274218, App
22	21	1.8	633	16	US-10-027-632-274218	Sequence 274218, App
23	21	1.8	76410	13	US-10-087-192-70	Sequence 70, Appl
24	21	1.8	220995	17	US-10-775-169-88	Sequence 88, Appl
25	20	1.7	248	15	US-10-029-386-25558	Sequence 25558, A
26	20	1.7	536	10	US-09-791-279-37	Sequence 37, Appl
27	20	1.7	543	15	US-10-029-386-11858	Sequence 11858, A
28	20	1.7	1053	15	US-10-112-356-6	Sequence 6, Appli
29	20	1.7	1085	16	US-10-305-720-1435	Sequence 1435, Ap
30	20	1.7	1326	17	US-10-398-036-19	Sequence 19, Appl
31	20	1.7	1552	13	US-10-027-632-263186	Sequence 263186,
32	20	1.7	1552	16	US-10-027-632-263186	Sequence 263186,
33	20	1.7	2049	15	US-10-235-567A-163	Sequence 163, App
34	20	1.7	2897	13	US-10-027-632-252125	Sequence 252125,
35	20	1.7	2897	16	US-10-027-632-252125	Sequence 252125,
36	19	1.6	355	10	US-09-814-353-5355	Sequence 5355, Ap
37	19	1.6	355	10	US-09-814-353-11642	Sequence 11642, A
38	19	1.6	415	10	US-09-814-353-18026	Sequence 18026, A
39	19	1.6	487	13	US-10-027-632-88455	Sequence 88455, A
40	19	1.6	487	13	US-10-027-632-307248	Sequence 307248,
41	19	1.6	487	16	US-10-027-632-88455	Sequence 88455, A
42	19	1.6	487	16	US-10-027-632-307248	Sequence 307248,
43	19	1.6	500	10	US-09-918-995-37950	Sequence 37950, A
44	19	1.6	531	9	US-09-893-737-21	Sequence 21, Appl
45	19	1.6	566	13	US-10-027-632-207090	Sequence 207090,

ALIGNMENTS

RESULT 1

US-10-283-975A-697
; Sequence 697, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 697
; LENGTH: 223
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(223)
; OTHER INFORMATION: N=any base
US-10-283-975A-697

Query Match 1.9%; Score 22; DB 17; Length 223;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCCACATTGTCCTTTCA 987
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Db 197 TCTGTTCCACATTGTCCTTTCA 218
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RESULT 2
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas W.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match          1.9%; Score 22; DB 9; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGCTCTTCA 987
Db 960 TCTGTTCAACAATTGCTCTTCA 981

RESULT 3
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match          1.9%; Score 22; DB 9; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGCTCTTCA 987
Db 960 TCTGTTCAACAATTGCTCTTCA 981

RESULT 4
US-10-349-253A-1
; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
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; SEQ ID NO 1
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; ORGANISM: Homo sapien
US-10-349-253A-1

Query Match          1.9%; Score 22; DB 13; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGCTCTTCA 987
Db 960 TCTGTTCAACAATTGCTCTTCA 981

RESULT 5
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
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/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
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/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,293
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-875-076-13

Query Match 1.9%; Score 22; DB 13; Length 1173;
Best Local Similarity 100.0%; Pred.No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAAAATGTCCTTTCA 987
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Db 960 TCTGTTCAAAATGTCCTTTCA 981

RESULT 6
US-09-876-252-13
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/ Publication No. US20030018182A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Lehmann-Bruinsma, Karin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Kuoping
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Receptor
/ FILE REFERENCE: ARN-0054
/ CURRENT APPLICATION NUMBER: US/09/876,252
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1998-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12

/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/152,524
/ PRIOR FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: 60/151,114
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
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/ PRIOR FILING DATE: 1999-10-01
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/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ NUMBER OF SEQ ID NOS: 146
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-876-252-13

Query Match 1.9%; Score 22; DB 13; Length 1173;
Best Local Similarity 100.0%; Pred.No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 960 TCTGTTCAAAATGTCCTTTCA 981

RESULT 7
US-10-052-193-1
/ Sequence 1, Application US/10052193
/ Publication No. US20020132755A1
/ GENERAL INFORMATION:
/ APPLICANT: Pfizer, Inc.
/ TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
/ FILE REFERENCE: PC10963A
/ CURRENT APPLICATION NUMBER: US/10/052,193
/ CURRENT FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1

Query Match 1.9%; Score 22; DB 14; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

RESULT 8

US-10-290-078-26
; Sequence 26, Application US/102900078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MP12001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
US-10-290-078-26

Query Match 1.9%; Score 22; DB 15; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

RESULT 9

US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Query Match 1.9%; Score 22; DB 15; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

RESULT 10

US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

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Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

RESULT 11

US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.

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/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/10/393,807
/ PRIORITY FILING DATE: 2003-03-21
/ PRIOR APPLICATION NUMBER: US/09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-393-807-13

Query Match      1.9%; Score 22; DB 15; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAAAATGTCCTTTCA 987
Db 960 TCTGTTCAAAATGTCCTTTCA 981

RESULT 12
US-10-417-820A-13
/ Sequence 13, Application US/10417820A
/ Publication No. US20030229216A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lowitz, Kevin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Behan, Dominic P.
/ TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: 7.US28.CON
/ CURRENT APPLICATION NUMBER: US/10/417,820A
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-417-820A-13
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/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match      1.9%; Score 22; DB 16; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAAAATGTCCTTTCA 987
Db 960 TCTGTTCAAAATGTCCTTTCA 981

RESULT 13
US-10-723-955-13
/ Sequence 13, Application US/10723955
/ Publication No. US20040110238A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lehman-Bruinsma, Karin
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Dang, Huang T.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Gore, Martin
/ APPLICANT: White, Carol
/ TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: 7.US29.CON
/ CURRENT APPLICATION NUMBER: US/10/723,955
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: 10/417,820
/ PRIOR FILING DATE: 2003-4-16
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-723-955-13
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Query Match 1.9%; Score 22; DB 17; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 960 TCTGTTTCAACAATTGTCCTTTCA 981

RESULT 14

US-10-737-619-1
; Sequence 1, Application US/10737619
; Publication No. US20040138234A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/737,619
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-619-1

Query Match 1.9%; Score 22; DB 17; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTTCAACAATTGTCCTTTCA 987
Db 960 TCTGTTTCAACAATTGTCCTTTCA 981

RESULT 15

US-10-782-596-13
; Sequence 13, Application US/10782596
; Publication No. US20040137509A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/782,596
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/875,076
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-782-596-13

Query Match 1.9%; Score 22; DB 17; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 960 TCTGTTTCAACAATTGTCCTTTCA 981

Search completed: October 1, 2004, 20:18:26
Job time : 664 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 14:37:09 ; Search time 3518 seconds

(without alignments)

9982.355 Million cell updates/sec

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Perfect score: 1176

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Searched: 27513289 seqs, 14931090276 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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1: em_estba.*

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10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

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26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	22	1.9	764	29	BB418962 BB418962
					CC584203 CH240_380

C 5	21	1.8	331	29	CE700949
C 6	21	1.8	602	28	AQ390595
C 7	21	1.8	722	28	CE849215
8	21	1.8	861	29	BZ227627
9	21	1.8	869	29	AY405330
10	21	1.8	869	29	AY405331
11	21	1.8	1023	12	BG563625
12	21	1.8	1103	14	CF661120
13	20	1.7	251	9	AZ250969
C 14	20	1.7	271	28	AZ491769
C 15	20	1.7	279	14	CB981626
C 16	20	1.7	360	14	D70276
C 17	20	1.7	360	14	D70608
C 18	20	1.7	373	13	C69245
C 19	20	1.7	418	28	CE642921
C 20	20	1.7	465	28	AZ150613
C 21	20	1.7	485	28	AQ181200
C 22	20	1.7	525	9	AL375854
C 23	20	1.7	528	29	CE738419
C 24	20	1.7	537	28	BH501816
C 25	20	1.7	539	12	BG906643
C 26	20	1.7	547	28	BZ473862
C 27	20	1.7	550	10	BF056033
C 28	20	1.7	567	28	AZ250002
C 29	20	1.7	575	12	BJ152289
C 30	20	1.7	592	28	BH289608
C 31	20	1.7	617	28	AZ559416
C 32	20	1.7	623	14	CB348956
C 33	20	1.7	632	14	CB349043
C 34	20	1.7	636	9	AU217737
C 35	20	1.7	636	29	CG960774
C 36	20	1.7	650	28	AZ471542
C 37	20	1.7	654	14	CB914678
C 38	20	1.7	660	28	BZ050817
C 39	20	1.7	676	28	BZ392492
C 40	20	1.7	684	28	BH987629
C 41	20	1.7	686	29	CG752731
C 42	20	1.7	687	14	CF538979
C 43	20	1.7	697	28	AZ381267
C 44	20	1.7	699	14	CA375189
C 45	20	1.7	704	14	CF147821

ALIGNMENTS

RESULT 1
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LOCUS
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DEFINITION
CG392906
ZMMBCC0004All 5', genomic survey sequence.
ACCESSION
CG392906
VERSION
CG392906.1 GI:34336131
KEYWORDS
GSS.
SOURCE
Zea mays subsp. mays (maize)
ORGANISM
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 997)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzaud,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGR (2003b)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7

Class: BAC ends
High quality sequence start: 97.
FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:4578"
/clone="ZMMBCC0004A11"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBCC (ECORI)"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI"

ORIGIN

Query Match 2.0%; Score 23; DB 29; Length 997;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 57 ATTTTAAATGCTTCATTGGCT 79
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Db 402 ATTTTAAATGCTTCATTGGCT 424
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RESULT 2

CC226484/c
LOCUS
DEFINITION
CH261-69015_RM1.1 CH261 Gallus gallus genomic clone CH261-69015,
genomic survey sequence.

ACCSSION
CC226484

VERSION
CC226484.1 GI:30553147

KEYWORDS
GSS.

SOURCE
Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
1 (bases 1 to 1051)

Warren, W., Graves, T., Mardis, E. and Wilson, R.

Gallus gallus BAC End Reads

Unpublished (2003)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 182000 Std Error: 0.00

Seq primer: RM1 TAGCATCTACTATAGGAGA

Class: BAC ends

High quality sequence start: 19

High quality sequence stop: 360.

FEATURES
source
1. .1051
Location/Qualifiers

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/mol_type="genomic DNA"

/strain="Red Jungle Fowl"

/db_xref="taxon:9031"

/clone="CH261-69015"

/sex="female"

/cell_line="UCD001, inbred 256"

/clone_lib="CH261"

/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;

CH261 Female Chicken library - For library and clone

ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 2.0%; Score 23; DB 28; Length 1051;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 849 AATTATTTTCTTCTTAATTGGC 827
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RESULT 3

BB418962

LOCUS

DEFINITION

BB418962

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 274)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,

Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,

Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,

Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,

Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,

Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Sugahara, Y., Suzuki, H., Tsunoda, Y., Watanabe, A.,

Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,

Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and

Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)

Unpublished (2000)

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,

Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermotabilization and thermostabilization of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Katsunai, T., Akiyama, J., Shibata, Y., Ozawa, Y., Muramatsu, M.,

Tomaru, Y., Carninci, P., Shibata, Y.,

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

FEATURES
source
1. .274
Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="C530014D15"

/tissue_type="spinal cord"

/dev_stage="12 days embryo"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 12 days embryo

spinal cord"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

BB418962 274 bp mRNA linear EST 16-JUL-2000
BB418962 RIKEN full-length enriched, 12 days embryo spinal cord Mus
musculus cDNA clone C530014D15 3' similar to APl17947 Homo sapiens
P2Z domain-containing guanine nucleotide exchange factor 1 mRNA,
mRNA sequence.

BB418962

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 274)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,

Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,

Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,

Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,

Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,

Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Sugahara, Y., Suzuki, H., Tsunoda, Y., Watanabe, A.,

Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,

Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and

Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)

Unpublished (2000)

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,

Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermotabilization and thermostabilization of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Katsunai, T., Akiyama, J., Shibata, Y., Ozawa, Y., Muramatsu, M.,

Tomaru, Y., Carninci, P., Shibata, Y.,

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

FEATURES
source
1. .274
Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="C530014D15"

/tissue_type="spinal cord"

/dev_stage="12 days embryo"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 12 days embryo

spinal cord"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

Library (Male) produced by Pieter de Jong"

Query Match 1.9%; Score 22; DB 29; Length 764;
Best Local Similarity 100.0%; Pred.No. 9.9;
Matches 22; Conservative 0; Mismatches 0; Indels

QY 370 GCTCAACACACTGGCATCATGA 391
|||
Db 635 GCTCAACACACTGGCATCATGA 614

RESULT 5	CE700949/c	CE700949	331 bp	DNA	linear	GSS 29-SEP-2003
LOCUS						
DEFINITION						tigr-gss-dog-17000368904282 Dog Library Canis familiaris genomic, genomic survey sequence.

CE/00949.1 GI:3/020173
GSS.
Canis familiaris (dog)
Canis familiaris

REFERENCE
1 (bases 1 to 331)
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.

AQ390595/c
 LOCUS
 CITR1-EI-2544B13.TR CITR1-EI Homo sapiens genomic clone 2544B13,
 602 bp DNA linear GSS 06-MAR-1999
 genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 602)

AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other GSs: CITBI-E1-2544B13.TF

Contact: Shaying Zhao, William Nierman, Mark Adams

The Institute for Eukaryotic Genomics

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES

source

1. .602

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="2544B13"

/sex="male"

/cell_type="sperm"

/clone_lib="CITBI-E1"

/notes="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;

CalTech Human BAC Library D"

ORIGIN

Query Match 1.8%; Score 21; DB 28; Length 602;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 640 AGCCATGCTGGATTCCTCACT 660

|||||

Db 498 AGCCATGCTGGATTCCTCACT 478

RESULT 7

CE849215/c

LOCUS

722 bp DNA linear GSS 01-OCT-2003

tigr-gss-dog-1700032984147 Dog Library Canis familiaris genomic,

genomic survey sequence.

CE849215

CE849215.1 GI:37214951

GSS.

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 722)

Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,

Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and

Venter,J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

14512627

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1. .722

/organism="Canis familiaris"

/mol_type="genomic DNA"

/strain="Standard Foodle"

FEATURES

source

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site_1: BstXI; Libraries were prepared from

peripheral blood"

ORIGIN

Query Match 1.8%; Score 21; DB 29; Length 722;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GAAGTAATATTTTCTTA 166

|||||

Db 188 GAAGTAATATTTTCTTA 168

RESULT 8

BZ227627

LOCUS

861 bp DNA linear GSS 12-OCT-2002

CH230-400N17.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone

CH230-400N17, genomic survey sequence.

BZ227627

BZ227627.1 GI:23886168

GSS.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 861)

Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,

Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,

Riggs,F., de Jong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 MboI segment

Unpublished (1999)

Other GSs: CH230-400N17.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/orering_information.htm). BAC end

page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 400 row: N column: 17

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .861

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/strain="BN/SsNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-400N17"

/sex="Female"

/cell_type="Brain"

/clone_lib="CHORI-230 Segment 2"

/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;

CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by

Pieter de Jong"

ORIGIN

Query Match 1.8%; Score 21; DB 28; Length 861;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TTGTATTCATTCCTCTGTA 215

|||||

Db 452 TTGTATTCATTCCTCTGTA 472

```

RESULT 9
AY405330
LOCUS
DEFINITION Homo sapiens MTNR1A gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY405330
VERSION AY405330.1 GI:39761304
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source
Location/Qualifiers
1..869
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM2188"

gene

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

```

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REFERENCE 2 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source
Location/Qualifiers
1..869
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>869
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/locus_tag="HCM2188"

gene

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1023)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1548 row: k column: 18
High quality sequence stop: 502.
Location/Qualifiers
1..1023
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4710281"
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/clone_lib="NIH_MGC_76"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctggcc); Site_2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,

```

CA). Note: this is a NIH_MGC Library."

```
ORIGIN
Query Match      1.8%; Score 21; DB 12; Length 1023;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 TAATATTATTTTCTTAATT 170
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Db 720 TAATATTATTTTCTTAATT 700

RESULT 12
CF661120      1103 bp mRNA linear EST 07-OCT-2003
DEFINITION    CcLL10a33n22f1 Carp liver library 5 Cyprinus carpio cDNA clone
33n22 5', mRNA sequence.
ACCESSION     CF661120
VERSION       CF661120
KEYWORDS      EST.
SOURCE        CF661120.1 GI:37558249
ORGANISM      Cyprinus carpio (common carp)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE     1 (bases 1 to 1103)
AUTHORS      Gracey,A.Y., Fraser,E., Li,W. and Cossins,A.R.
TITLE        Microarray and EST analysis of the carp (Cyprinus carpio)
transcriptome during environmental stress
JOURNAL       Unpublished (2003)
COMMENT       Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44 (0)151-795-4510
Fax: +44 (0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 33 row: n column: 22
Seq primer: Triplex 5' LD (5'-CTCGGAGCGGCCCATCTGTGTGT-3')
High quality sequence start: 35
High quality sequence stop: 830.
FEATURES      Location/Qualifiers
source        1..1103
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/db_xref="taxon:7962"
/clone="33n22"
/sex="Male & female"
/tissue_type="Liver"
/dev_stage="Adult"
/lab_host="E.coli Electronax DH10B"
/clone_lib="Carp liver library 5"
/notes="Vector: pTriplex2; Site 1: Sfil GGCCATTAGCGCC;
Site 2: Sfil GGCGCTCGGCC; Serially subtracted cDNA
library prepared from liver of warm, cold and hypoxia
challenged animals"

ORIGIN
Query Match      1.8%; Score 21; DB 14; Length 1103;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 540 AATGCTCTTGAATTCCTGCT 560
|||||
Db 214 AATGCTCTTGAATTCCTGCT 234

RESULT 13
AA250969      251 bp mRNA linear EST 13-AUG-1997
LOCUS         z507a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684524 3'
DEFINITION
```

```
similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION     AA250969
VERSION       AA250969.1 GI:1885930
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 251)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
Email: rgapbs-rc@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 245.
FEATURES      Location/Qualifiers
source        1..251
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:684524"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP GCB1"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAATGGAGCGCGCTCATTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Donaldo."

ORIGIN
Query Match      1.7%; Score 20; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 GCCAGGTCACTGGCCATCCT 929
|||||
Db 173 GCCAGGTCACTGGCCATCCT 192

RESULT 14
AA2491769/c
LOCUS         AZ491769
DEFINITION    1M0325H05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0325H05 R, genomic survey sequence.
ACCESSION     AZ491769
VERSION       AZ491769.1 GI:10663795
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 271)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
```


University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0325 row: H column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 271.

Location/Qualifiers
1. 271
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0325H05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.

Location/Qualifiers

1. 279

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB70005_IIIAF_B07"
/sex="Hermaphrodite"
/dev_stage="Post-Veraison, 18-19 brix"
/lab_host="DH5alpha"
/clone_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"
/note="Organ: Berry; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGGTATCAACGACAGTGGCATTACGGCGGG-3' and 5'-ATTCTAGAGCGGCGGCGCATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 1.7%; Score 20; DB 14; Length 279;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 822 TGCCTTCAAAGTGGGTTCT 841
|||||
Db 61 TGCCTTCAAAGTGGGTTCT 42
|||||

Search completed: October 1, 2004, 18:37:41
Job time : 3527 secs

Query Match 1.7%; Score 20; DB 28; Length 271;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 195 TTGATTCCATTCCTCTGT 214
|||||
Db 127 TTGATTCCATTCCTCTGT 108
|||||

RESULT 15
CB981626/c
LOCUS CB981626 279 bp mRNA linear EST 01-MAY-2003
DEFINITION CAB70005_IIIAF_B07 Cabernet Sauvignon Berry Post-Veraison - CAB7
Vitis vinifera cDNA clone CAB70005_IIIAF_B07 5', mRNA sequence.
ACCESSION CB981626
VERSION CB981626.1 GI:30304832
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 279)
AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and Cook, D.
TITLE Expressed sequence tags from cabernet sauvignon berries at various developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Douglas Cook, PhD
CAES Genome Facility

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 10:05:02 ; Search time 59 Seconds
(without alignments)
1872.476 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAISQNSQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	99.4	391	5	AAM50565 Mouse his
2	1745	85.2	391	5	AAM50566 Rat hist
3	1370.5	66.9	390	3	AAB02831 Human G p
4	1370.5	66.9	390	3	AAV71297 Human orp
5	1370.5	66.9	390	4	AAE62445 Human GPC
6	1370.5	66.9	390	4	AAE64477 Human G p
7	1370.5	66.9	390	4	AAE64477 Human G p
8	1370.5	66.9	390	4	AAE64477 Human G p
9	1370.5	66.9	390	5	AAM53050 Human G p
10	1370.5	66.9	390	5	ABP98629 Human his
11	1370.5	66.9	390	5	ABP78276 Amino aci
12	1370.5	66.9	390	5	AAM50564 Human his
13	1370.5	66.9	390	5	AAE66023 Human his
14	1370.5	66.9	390	6	AAU74906 Amino aci
15	1370.5	66.9	390	6	ABG71960 Human G-p
16	1370.5	66.9	390	6	ABU92265 Human G p
17	1370.5	66.9	390	6	ABP81727 Human his
18	1370.5	66.9	390	6	AAE36417 Human his
19	1370.5	66.9	390	5	AAM53052 Human G p
20	1370.5	66.9	390	5	AAM53053 Human G p
21	1366.5	66.7	390	4	AAM51410 Human GPR
22	1366.5	66.7	390	6	AAE36416 Human H4
23	1238	60.4	389	5	AAM50567 Guinea pi
24	1198	58.5	357	6	AAE36415 Human H4
25	1074.5	52.5	336	6	AAE36414 Human H4
26	729.5	35.6	415	7	AAO29530 Human H3

26	722.5	35.3	445	2	AAW92975	Aaw92975 Human mAC
27	722.5	35.3	445	2	AAW92975	Aay06322 Human G p
28	722.5	35.3	445	2	AAW92975	Aag67830 Human his
29	722.5	35.3	445	3	AAW92218	Aay92218 Human his
30	722.5	35.3	445	4	AAW92218	Aab30627 A human h
31	722.5	35.3	445	5	ABB79792	Abb79792 Human his
32	722.5	35.3	445	6	ABR43667	Abp57425 Human his
33	722.5	35.3	445	6	ABP57425	Abp57425 Human his
34	722.5	35.3	445	6	AAO19746	Aao19746 Human his
35	722.5	35.3	445	6	ABP81687	Abp81687 Human his
36	722.5	35.3	445	6	ABG74567	Abg74567 Human his
37	722.5	35.3	445	6	ABG74567	Abg74567 Human his
38	722.5	35.3	445	6	ABP59931	Abp59931 Human his
39	722.5	35.3	445	7	AAO29527	Aao29527 Human wil
40	722.5	35.3	445	7	ADD22854	Add22854 Human his
41	722.5	35.3	453	2	AAW22208	Aay22208 Human G-p
42	722.5	35.3	453	3	AAW15381	Aab15381 Human G-p
43	719.5	35.1	449	4	ABG12680	Abg12680 Novel hum
44	718.5	35.1	445	6	ABR43668	Abp57426 Monkey hi
45	718.5	35.1	445	6	ABP57426	Abp57426 Monkey hi

ALIGNMENTS

RESULT 1
AAM50565
ID AAM50565 standard; protein; 391 AA.
XX AC AAM50565;
XX AC
XX 18-MAR-2002 (first entry)
XX DT
XX DE Mouse histamine H4 receptor.
XX KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
XX KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
XX KW diagnosis; gene therapy.
XX OS Mus musculus.
XX PN WO200192485-A1.
XX PD 06-DEC-2001.
XX PF 22-FEB-2001; 2001WO-US005914.
XX PR 31-MAY-2000; 2000US-0208260P.
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX PI Lovenberg T, Liu C;
XX DR WPI; 2002-114339/15.
XX DR N-PSDB; AAI70981.
XX DR New mammalian histamine H4 receptor proteins and polynucleotides encoding
XX PT the proteins, useful in gene therapy for treating diseases where it is
XX PT beneficial to elevate mammalian histamine H4 receptor activity.
XX PS Claim 13; Fig 5B; 92pp; English.
XX CC The present sequence is that of a mouse histamine receptor of the H4
XX CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA
XX CC library. The invention provides mammalian (human, mouse, rat and guinea
XX CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
XX CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
XX CC recombinant host cells that produce active recombinant protein. The
XX CC pharmacology of known histamine ligands is demonstrated. Mammalian
XX CC histamine H4 receptor may be used in gene therapy for the treatment of
XX CC diseases where it is beneficial to elevate mammalian histamine H4
XX CC receptor activity. Recombinant protein is useful for identifying
XX CC modulators of the histamine H4 receptor. Such modulators may be useful

CC for diagnosing, treating or preventing asthma, allergy, inflammation,
CC cardiovascular and cerebrovascular disorders, non-insulin dependent
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
CC the neuroendocrine system, stress and spasticity
XX
SQ Sequence 391 AA;

Query Match 99.4%; Score 2035; DB 5; Length 391;
Best Local Similarity 99.7%; Pred. No. 1.9e-202;
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNHRSNFFFLNLAIS 60
Db 1 MSESNSGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNHRSNFFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPHLVFNMFNGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPHLVFNMFNGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120

Qy 121 SYRAQHTGIMKIVAQVAVWILAFVNGPMLASDSWKNSNTKDCPEGFVTEWYILIT 180
Db 121 SYRAQHTGIMKIVAQVAVWILAFVNGPMLASDSWKNSNTKDCPEGFVTEWYILIT 180

Qy 181 MLEFLLPVIISVAVFNVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHAGVACRTSN 240
Db 181 MLEFLLPVIISVAVFNVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHAGVACRTSN 240

Qy 241 PGLKESAAHSRHSPPRRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILRG 300
Db 241 PGLKESAAHSRHSPPRRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILRG 300

Qy 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSFVNPFY 360
Db 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSFVNPFY 360

Qy 361 PLCHRRFOKAFWKILCVTKQPALSONQSVSS 391
Db 361 PLCHRRFOKAFWKILCVTKQPALSONQSVSS 391

RESULT 2
AAM50566
ID AAM50566 standard; protein; 391 AA.
XX AC AAM50566;
DT 18-MAR-2002 (first entry)
XX XX
DE Rat histamine H4 receptor.
XX Histamine H4 receptor; rat; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy.
XX
OS Rattus rattus.
XX
PN WO200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T, Liu C;
XX
DR WPI; 2002-114339/15.
DR N-PSDB; AAI70982.
XX
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
the proteins, useful in gene therapy for treating diseases where it is

beneficial to elevate mammalian histamine H4 receptor activity.

Claim 13; Fig 6A; 92pp; English.

XX
XX
XX
CC The present sequence is that of a rat histamine receptor of the H4
CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA
CC library. The invention provides mammalian (human, mouse, rat and guinea
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC recombinant host cells that produce active recombinant protein. The
CC pharmacology of known histamine ligands is demonstrated. Mammalian
CC histamine H4 receptor may be used in gene therapy for the treatment of
CC diseases where it is beneficial to elevate mammalian histamine H4
CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the histamine H4 receptor. Such modulators may be useful
CC for diagnosing, treating or preventing asthma, allergy, inflammation,
CC cardiovascular and cerebrovascular disorders, non-insulin dependent
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
CC the neuroendocrine system, stress and spasticity
XX

Sequence 391 AA;

Query Match 85.2%; Score 1745; DB 5; Length 391;

Best Local Similarity 84.9%; Pred. No. 2.6e-172;
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNHRSNFFFLNLAIS 60

Db 1 MSESNGTDVLPHTAQVPLAFMSSLAFAITIGNAVVILAFVADNRNHRSNFFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPHLVFNMFNGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120

Db 61 DFPVGVISIPLYIPHTLFNMFNGSGICMFWLITDYLLCTASVYVILISYDRYQSVNAV 120

Qy 121 SYRAQHTGIMKIVAQVAVWILAFVNGPMLASDSWKNSNTKDCPEGFVTEWYILIT 180

Db 121 RYRAQHTGILKIVAQVAVWILAFVNGPMLASDSWKNSNTBECEGFVTEWYILIT 180

Qy 181 MLEFLLPVIISVAVFNVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHAGVACRTSN 240

Db 181 AFLEFLLPVLVYVFSQIYWSLWKSGLSRCPHAGFIATSSRGTGHSRRRTGLACRTSL 240

Qy 241 PGLKESAAHSRHSPPRRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILRG 300

Db 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGIIAFKVGSPFCRSESPVLHQREHVELLRG 300

Qy 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSFVNPFY 360

Db 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSLINFY 360

Qy 361 PLCHRRFOKAFWKILCVTKQPALSONQSVSS 391

Db 361 PLCHRRFOKAFWKILCVTKQAPAPSTQSVSS 391

RESULT 3

AAB02831

ID AAB02831 standard; protein; 390 AA.

XX AC AAB02831;

DT 22-AUG-2000 (first entry)

XX Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.

DE Human; G protein coupled receptor; GPCR; transmembrane receptor;

KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.

XX Homo sapiens.

XX WO200022131-A2.

XX 20-APR-2000.


```
QY 361 PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391
Db 359 PLCHKRFOKAFWKILCVTKWPAISQ-NQSVSS 390

RESULT 6
AAG64477
ID AAG64477 standard; protein; 390 AA.
XX
AC AAG64477;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human G protein-coupled receptor protein BG26.
XX
KW Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
KW altering intracellular cAMP concentration;
KW regulating signal transduction.
XX
OS Homo sapiens.
XX
PN WO200146414-A1.
XX
PD 28-JUN-2001.
XX
PF 20-DEC-2000; 2000WO-JP009038.
XX
PR 20-DEC-1999; 99JP-00361687.
XX
PA (BANY ) BANYU PHARM CO LTD.
XX
PI Itadani H, Nakamura T, Tanaka K, Ohta M;
XX
DR WPI: 2001-441675/47.
XX
DR N-PSDB; AA47911.
XX
PT G protein-coupled receptor protein BG26, with activity of binding to
PT histamine and capable of changing intracellular cAMP concentration in
PT response to its stimulus, applicable as tool in screening ligands or drug
PT candidates.
XX
PS Claim 1; Page 41-44; 50pp; Japanese.
XX
CC The present sequence is that of the human G protein-coupled receptor
CC protein BG26, which shows significant homology with histamine H3, with
CC activity of binding to histamine and capable of changing intracellular
CC cAMP concentration in response to its stimulus. The protein is applicable
CC as a tool in screening ligands or drug candidates for regulating signal
CC transduction from such protein and treating diseases associated with its
CC abnormality
XX
SQ Sequence 390 AA;
Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 2.1e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSENSTGILPPAAOVFLAFMSSFAFALMGNVAVILAFVVDNRHRSNFFFLNLAIS 60
Db 1 MPDTNSTNLSTRVTLLAFFMSLVAFALMGNALVILAFVVDNRHRSNFFFLNLAIS 60
QY 61 DFLVGLISILPIPHVLEFNWNGSGICMFWLITDYLCTASVYVNIILISYDRYQSVSNV 120
Db 61 DFFVGVISIPLVPHLTFEWDGKEICVFWLITDYLCTASVYVNIILISYDRYLSVNAV 120
QY 121 SYRAQHTGMKIVQAVWVILAFVNGPMILASDSWKNSTNTKDCPEGFVTEWILITIT 180
Db 121 SYRTQHTGVLKIVTLVAVWVILAFVNGPMILVSESWKDEGS-ECEPGFFSEWILAIT 178
QY 181 MLEFLLPVISVAYENVQIVYSLWKRALSRCPSHAGFTTSSSAGSHLHAGVACRTSN 240
Db 179 SFLERVIPVILVAYNMNIYSLWKRDLHLSRCQSHPLGTAVSSNICGHSFRGLSSRSL 238
```

```
QY 241 PGLKESAAHRSRSPRRKSSILVSLRTHKSSITAFKVGSWFSESAALRQREYAEILRG 300
Db 239 SASTVPASPHSRQRKSSIMFSSRTKMSNTIASKMGFSQSDSVLHQHREVELLA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTVILSTYPRTERPKSVWYSTAFWLQFNFSVNPPLY 360
Db 299 RRLAKSLAILLGVFVCAWAPYSFLTIVLSFYSSATGPKSVWYRIAFWLQFNFSVNPPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391
Db 359 PLCHKRFOKAFWKILCVTKWPAISQ-NQSVSS 390

RESULT 7
AAB73622
ID AAB73622 standard; protein; 390 AA.
XX
AC AAB73622;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human G protein-coupled receptor AXOR35.
XX
KW AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; depression; anxiety; schizophrenia;
KW manic depression; bipolar disorder; dyskinesia; Parkinson's disease;
KW severe mental retardation; Huntington's disease; Gilles de la Tourette's syndrome;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery.
XX
OS Homo sapiens.
XX
PN WO200133221-A1.
XX
PD 10-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029461.
XX
PR 02-NOV-1999; 99US-00431898.
XX
PR 03-FEB-2000; 2000US-00497790.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Aubart KM, Bergema DJ, Fitzgerald LR, Graybill TL, Li X;
PI Michalovich D, Morrow DM, Zhu Y;
XX
DR WPI: 2001-316464/33.
DR N-PSDB; AA424007.
XX
PT Novel G-protein coupled receptor polypeptide and polynucleotide for
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
PT disorders and for identifying modulators useful for treating asthma.
XX
PS Claim 1; Page 50-51; 54pp; English.
XX
CC The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
CC and nucleotides may be used to treat a wide variety of disorders
CC including bacterial, fungal, protozoal and viral infections, particularly
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HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR35 activity or expression. Such AXOR35 modulators are particularly useful for treating asthma, and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils or neutrophils in asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via the detection of mutations in the corresponding gene. AXOR35 proteins are also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nucleotides are also useful as diagnostic reagents, in chromosome localisation and tissue expression studies, and for producing transgenic animals useful in drug discovery. AXOR35-specific antibodies are useful for purifying the AXOR35 protein or fragments thereof, and are also useful for treating conditions associated with the expression of the AXOR35 protein. The present sequence represents human AXOR35

Sequence 390 AA;

Query Match	66.9%;	Score 1370.5;	DB 4;	Length 390;
Best Local Similarity	68.1%;	Pred. No. 2.1e-133;		
Matches 267;	Conservative 40;	Mismatches 82;	Indels 3;	Gaps 2
Qy	1	MSESNSTGILPPAAQVPLAFMLSPAFAMGVNAVILAFVVDRLNLRHSNYFFFLNLAIS	60	
Db	1	MPDTNSTINLSIRTVILAFPKSLVAFAPMLGNALVILAFVVDKLNLRHSYFFFLNLAIS	60	
Qy	61	DFLVGLSIPILYIPHLVFNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVSNV	120	
Db	61	DFVGVVISIPLYIPHTLPEWDFGKICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNV	120	
Qy	121	SYRAQHTGIMKIVQAQMAVILAFVANGPMILASDSWKNSTNTKDCPCGFVTEWYITLT	180	
Db	121	SYRQHTGVKIVITLMVAVILAFVANGPMILVLSWESKDEGS--ECPCGFFSEWYITLT	178	
Qy	181	MLLBFLLPVISVAVFNVQIYNSLWKRRRLRSCFESHAGFTSTSSAGHILHRAGVACRTSN	240	
Db	179	SFLFVIVPILVAYFNWNIYNSLWKRDHLRSCQSHPLTAVSSNICGHFSFRGLSSRRSL	238	
Qy	241	PGLKESAAARSISESPRRKSSILVSLRTHMNSSITAFKVGSPWRSSEAAALRQREYAEILRG	300	
Db	239	SASTEVPAFHSERQRRKSSLSMFSSRTKMNSNTIAASKMGFSQSDVALHQREHVELLRA	298	
Qy	301	RKLARSLAILLSAPALCNAPYCLFTVILSTYPRTERPKSVVYKSIAPFLQWFNSVFNPFY	360	
Db	299	RRLKSLAILLGVFVAVCNAPYSLFTVILSYFYSSATGPKSVWYRIAPFLQWFNSVFNPLY	358	
Qy	361	PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS	391	
Db	359	PLCHRRFOKATKIFCIKKOPIPLPSOHSRSVSS	390	

RESULT 8

RESULT 8
AAM53050

AA53050
TD AA53050 standard: protein: 390 AA.

XX
AC
ZAMS3050:

AC
XX
AAM53050;

XX
PT 26-MAR-2002 (first entry)

XX DE Human G protein-coupled receptor nGPCR-2067.

XX DE FUM

Human: nGPCR-2067; G protein-coupled receptor; 7TM receptor; KW

signal transduction; mental disorder; central nervous system disease; KW

metabolic disease; infection; HIV-1, HIV-2; pain; neurological disorder; psychotic disorder; Huntington's disease; schizophrenia; migraine; depression; anxiety; bipolar disorder; dementia; Alzheimer's disease; Parkinson's disease; proliferative disorder; cancer; psoriasis; benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia; thyroid disorder; cardiovascular disease; hypertension; hypertension; thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis; inflammatory conditions; autoimmune disorder; rheumatoid arthritis; hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic; antididiabetic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant; antiatherosclerotic; neuroleptic; antimigraine; antiParkinsonian; tranquiliser; antidepressant; neuroprotective; anticonvulsant; antinflammatory; antirheumatic; antiarthritic; antipsoriatic; gene therapy; receptor.

Homo sapiens.

Key	Location/Qualifiers
Domain	19. .41
	/label= Transmembrane_domain_1
Domain	52. .74
	/label= Transmembrane_domain_2
Domain	86. .110
	/label= Transmembrane_domain_3
Domain	128. .146
	/label= Transmembrane_domain_4
Domain	172. .194
	/label= Transmembrane_domain_5
Domain	305. .326
	/label= Transmembrane_domain_6
Domain	342. .360
	/label= Transmembrane_domain_7

WO200185793-A2.

15-NOV-2001.

08-MAY-2001: 2001WO-US014750.

08-MAY-2000; 2000US-0203108P.

(PHAA) PHARMACIA & UPJOHN CO.

Lind P., Seilitz T., Vogeli G, Wood LS;

WPT: 2002-062240/08.

WET; 2002-062240/
N-PSDB: ABA02496.

New polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encodes the novel G protein-coupled receptor (NGPCR-2067).

Claim 31: Page 63: 100nm: English:

This sequence represents a novel human G protein-coupled receptor (GPCR) designated NGPCR-2067. Like all GPCRs, NGPCR-2067 has 7 putative transmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding NGPCR-2067, to recombinant expression of NGPCR-2067, to antibodies specific for NGPCR-2067, to drug screening methods that use NGPCR-2067, and to modulators of NGPCR-2067 activity. NGPCR-2067 nucleic acid sequences may be used to isolate NGPCR-2067 allelic variants and species homologues and may also be used in genetic mapping. The invention also discloses the use of NGPCR-2067 nucleic acids in screening for a predisposition to NGPCR-2067-associated hereditary mental disorders, or for the diagnosis of these disorders. NGPCR-2067 nucleic acids may additionally be used to generate transgenic animals, including knockout animals, which may provide an insight into treating a variety of human disorders, and may also be used in the design of antisense molecules for suppressing expression of NGPCR-2067 in cells. NGPCR-2067, and NGPCR-2067 modulators may be used to treat a wide variety of medical conditions, particularly mental disorders, central nervous system diseases, and metabolic diseases. Diseases that may be treated include

```
CC viral infections, particularly HIV-1 or HIV-2 infections; pain; central
CC nervous system, neurological and psychotic disorders such as Huntington's
CC disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,
CC dementia, Alzheimer's disease, and Parkinson's disease; proliferative
CC disorders such as cancers, benign prostatic hypertrophy and psoriasis;
CC metabolic disorders such as diabetes, dyslipidaemia, obesity, and
CC anorexia; thyroid disorders; cardiovascular diseases such as hypotension,
CC hypertension, thrombosis, myocardial infarction, cardiomyopathies, and
CC atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
CC rheumatoid arthritis); hormonal disorders; and renal failure
XX Sequence 390 AA;
SQ
Query Match 66.9%; Score 1370.5; DB 5; Length 390;
Best Local Similarity 68.1%; Pred. No. 2.1e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSESNTGILPPAAQVPLAFMLSSFAFAMVGNVAVILAFVVDNRNLRHSNYPFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLAFVSLVAFALMGNALVILAFVVDKNLRHSSYFFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFVNNFGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHLFVNDGFKICVFWLTDTYLLCTASVNVNVLISYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIVAOVAVVILAFVNGPMLASDSWKNSTNTKDCPEPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVVILAFVNGPMLVSVESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAYFNNIYWSLWKRDLHLSRCQSHPLGTAVSSNICHSFRLSSRRSL 238
QY 241 PGLKESAAARHSESPPRKSSILVSLTHMNSSITAFKVGSMFSESAAALRQREYAEILRG 300
Db 239 SASTVEVPASFHSEQRQRKSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYVYAFWLOWFNSFVNPLY 360
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO--NQSVSS 391
Db 359 PLCHRRFQKAFKIFCIKQPLPSOHSRSVSS 390
RESULT 9
ABP98629
ID ABP98629 standard; protein; 390 AA.
XX AC ABP98629;
XX
13-JUN-2003 (first entry)
DE Human histamine receptor SP9144.
XX
KW human; histamine receptor; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
KW psoriasis; receptor.
XX
OS Homo sapiens.
XX
PN US6204017-B1.
XX
PD 20-MAR-2001.
XX
PF 07-OCT-1999; 99US-00414010.
XX
PR 07-OCT-1999; 99US-00414010.
```

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XX (SCHE ) SCHERING CORP.
PA Behan JX, Hedrick JA, Laz TM, Mousma FJ, Morse KL, Umland SP;
XX Wang S;
XX WPI; 2002-442063/47.
DR N-PSDB; ABZ80663.
XX
PT New nucleic acid encoding antigenic part of human histamine receptor,
PT useful for preparing antibodies, e.g. for treating-histamine related
PT disorders.
XX
XX Example 1; Col 27-30; 19pp; English.
XX
CC This sequence represents the amino acid sequence of a human histamine
CC receptor (HR) designated SP9144. The sequence was isolated by searching
CC databases with the sequence of known G-coupled protein receptor (GPCR).
CC The gene is used for recombinant production of HR and for preparing
CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity
CC chromatography, in immunoassay of histamine receptor, to identify cDNA
CC clones that express the receptor, as antagonist to block binding of
CC histamine (for treating any histamine-associated disorder) and to
CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR
CC protein can be used in the treatment of e.g. inflammation, asthma,
CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
CC sclerosis, inflammatory bowel disease and psoriasis
XX
XX Sequence 390 AA;
Query Match 66.9%; Score 1370.5; DB 5; Length 390;
Best Local Similarity 68.1%; Pred. No. 2.1e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSESNTGILPPAAQVPLAFMLSSFAFAMVGNVAVILAFVVDNRNLRHSNYPFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLAFVSLVAFALMGNALVILAFVVDKNLRHSSYFFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFVNNFGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHLFVNDGFKICVFWLTDTYLLCTASVNVNVLISYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIVAOVAVVILAFVNGPMLASDSWKNSTNTKDCPEPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVVILAFVNGPMLVSVESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAYFNNIYWSLWKRDLHLSRCQSHPLGTAVSSNICHSFRLSSRRSL 238
QY 241 PGLKESAAARHSESPPRKSSILVSLTHMNSSITAFKVGSMFSESAAALRQREYAEILRG 300
Db 239 SASTVEVPASFHSEQRQRKSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYVYAFWLOWFNSFVNPLY 360
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO--NQSVSS 391
Db 359 PLCHRRFQKAFKIFCIKQPLPSOHSRSVSS 390
RESULT 10
ABB78276
ID ABB78276 standard; protein; 390 AA.
XX AC ABB78276;
XX
05-DEC-2002 (first entry)
XX
DE Amino acid sequence of human histamine receptor.
```

XX KW Human; histamine receptor; receptor; inflammation; asthma; allergy;
 KW atopic dermatitis; stroke; myocardial infection; migraine;
 KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;
 KW multiple sclerosis; inflammatory bowel disease; psoriasis;
 KW intracellular second messenger pathway; cellular growth rate;
 KW hormone secretion.
 XX OS Homo sapiens.
 XX XX US2002098539-A1.
 XX XX 25-JUL-2002.
 XX XX 19-MAR-2001; 2001US-00812216.
 XX XX 07-OCT-1999; 99US-00414010.
 XX XX (BEHA/) BEHAN J X.
 XX XX (HEDR/) HEDRICK J A.
 XX XX (LAZT/) LAZ T M.
 XX XX (MONS/) MONSMA F J.
 XX XX (MORS/) MORSE K L.
 XX XX (UNLA/) UMLAND S P.
 XX XX (WANG/) WANG S.
 XX XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;
 XX Wang S;
 XX WPI; 2002-673827/72.
 XX N-PSDB; ABW78739.
 XX Novel mammalian histamine receptor polypeptide useful for identifying
 XX agonist or antagonist for treating diseases such as inflammation, asthma,
 XX stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
 XX Claim 2; Page 16-17; 21pp; English.
 XX The present sequence represents a histamine receptor. The polypeptide is
 XX useful for identifying an agonist or antagonist of a mammalian histamine
 XX receptor. It is useful as an antigen to elicit the production of
 XX antibodies. The histamine receptor polypeptide and polynucleotide are
 XX useful in the treatment and management of diseases such as inflammation,
 XX asthma, allergy, atopic dermatitis, stroke, myocardial infection,
 XX migraine, chronic obstructive pulmonary disease (COPD), rheumatoid
 XX arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
 XX They are also useful for modulating intracellular second messenger
 XX pathway activated through histamine receptors (cyclic-AMP, calcium,
 XX inositol phosphate and mitogen activated protein (MAP) kinase), changes
 XX in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
 XX mobilization, mitogenic effects, etc
 XX SQ Sequence 390 AA;
 Query Match 66.9%; Score 1370.5; DB 5; Length 390;
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
 QY 1 MSENSTGILPPAAQVPLAFIMSSFAFAMVGNVAVILAFVVDRLNRHSNFFNLAIS 60
 Db 1 MPDTNSTINLSLSTRVTLFAFFMSLVAFALMLGNALVILAFVVDKLRHSNFFNLAIS 60
 QY 61 DELUGLISIPLYIPIHVNFRSGTCMPWLTVDLLCTASVYINVLISYDRYSQVSNV 120
 Db 61 DFFVGVISIPIHPTLFEWDFGKEICVFWLTVDLLCTASVYINVLISYDRYSQVSNV 120
 QY 121 SYRAQHTGIMKTVQAVQVAVILAFVNGPMLASDSWKNSTNTKDCPGFVTEWILIT 180
 Db 121 SYRTQHTGVKLVTLMVAVVILAFVNGPMLVSVESWKEGS--BCEPGFFSEWILAIT 178
 QY 181 MLLEFLLPVISVAYFNQVYIWSLWKRRLSRCEPSHAGFTSTSSASGHLHAGVACRTSN 240
 Db 179 SPLEFVIPVILVAYFNMNIYWSLWKRDLHLSRCQSHPLGLTAVSSNIGHSFRGLSSRRSL 238

241 PGLKGAASRHSRPRKSSILVSLRTHMNSSITAFKVSFWRSESAALRQREYAEILRG 300
 239 SATEVPASHFSERQQRKSSLMFSSRTKMSNTIASQWGSFSQSDSVLHQREHVELRA 298
 301 RKLARSLAILLSAPACWAPYCLFTIVLSTYPTERTPKSVYYSIAFWLQWNSFNPFY 360
 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVMYRIAFWLFQWNSFNPFY 358
 361 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 391
 359 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 11
 AAM50564
 ID AAM50564 standard; protein; 390 AA.
 XX AC AAM50564;
 XX DT 18-MAR-2002 (first entry)
 XX DE Human histamine H4 receptor.
 XX KW Histamine H4 receptor; human; antiasthmatic; antiallergenic;
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
 KW diagnosis; gene therapy.
 XX OS Homo sapiens.
 XX OS WO200192485-A1.
 XX PD 06-DEC-2001.
 XX PF 22-FEB-2001; 2001WO-US005914.
 XX PR 31-MAY-2000; 2000US-0208260P.
 XX PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX PI Lovenberg T, Liu C;
 XX WPI; 2002-114339/15.
 XX N-PSDB; AAI70980.
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
 XX the proteins, useful in gene therapy for treating diseases where it is
 XX beneficial to elevate mammalian histamine H4 receptor activity.
 XX Claim 13; Fig 2; 92pp; English.
 XX The present sequence is that of a human histamine receptor of the H4
 XX subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA
 XX library. The invention provides mammalian (human, mouse, rat and guinea
 XX pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
 XX polypeptides (see AAM50564-67). The nucleic acids have been expressed in
 XX recombinant host cells that produce active recombinant protein. The
 XX pharmacology of known histamine ligands is demonstrated. Mammalian
 XX histamine H4 receptor may be used in gene therapy for the treatment of
 XX diseases where it is beneficial to elevate mammalian histamine H4
 XX receptor activity. Recombinant protein is useful for identifying
 XX modulators of the human histamine H4 receptor. Such modulators may be
 XX useful for diagnosing, treating or preventing asthma, allergy,
 XX inflammation, cardiovascular and cerebrovascular disorders, non-insulin
 XX dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
 XX disorders of the neuroendocrine system, stress and spasticity
 XX SQ Sequence 390 AA;
 Query Match 66.9%; Score 1370.5; DB 5; Length 390;
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

```
QY 1 MSENSTGILPPAAQVPLAFMSFPAFAIMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
1 MPDTNSTINLSLSTRVTLAFMSLVAFALMGNALVILAFVVDKRLHRSSYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVSNV 120
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYVNLISYDRYLSVSNV 120
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLIASDSWKNSTNTKDCBPGFVTEWYILIT 180
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
121 SYRTQHTGVLKIVTLMAVAVILAFVNGPMLLVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLLEFLLPVISVAYENVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
179 SFLEFVIPVILVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSITAFKVGFSWSESAAALQREYAEALLRG 300
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
239 SASTEPVASFHSEQRQRKSSLMFSSRTVMNSITASKMGFSQSDSVVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSVNPFLY 360
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
299 RRLAKSLAILLGVAFVCAWAPYSLFTIVLSYSSATGPKSVWYRIAFWLQFNFSVNPFLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 391
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
359 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 12
AAG66023
ID AAG66023 standard; protein; 390 AA.
AC
XX
XX
27-FEB-2002 (first entry)
XX
DE Human histamine H4 receptor protein.
XX
KW Histamine receptor; H4; anti-rheumatic; anti-arthritis; immunosuppressive;
KW antiasthmatic; antiallergic; neuroprotective; antidiabetic; human;
KW cerebroprotective; CAMP modulator; gene therapy.
OS Homo sapiens.
XX
FH Key
FT 12..40
FT Domain
FT /note= "transmembrane domain"
FT 52..69
FT Domain
FT /note= "transmembrane domain"
FT 88..110
FT Domain
FT /note= "transmembrane domain"
FT 130..154
FT Domain
FT /note= "transmembrane domain"
FT 172..196
FT Domain
FT /note= "transmembrane domain"
FT 304..325
FT Domain
FT /note= "transmembrane domain"
FT 342..362
FT Domain
FT /note= "transmembrane domain"
XX
PN WO200185786-A2.
XX
XX
XX 15-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US014527.
XX
XX 05-MAY-2000; 2000US-0202151P.
XX 23-AUG-2000; 2000US-0227567P.
XX 13-NOV-2000; 2000US-0247855P.
XX
XX (AMHP ) AMERICAN HOME PROD CORP.
XX
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PI Jones PG, Blatcher M, Wu S, Pausch MH;
XX WPI; 2002-049442/06.
DR N-PSDB; AAI67750.
XX
PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
PT for treating transplanted organ rejection, asthma, allergy, multiple
PT sclerosis and rheumatoid arthritis.
XX
XX Claim 5; Fig 1; 66pp; English.
XX
CC The invention provides an isolated histamine receptor, H4, which binds
CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
CC receptor can be expressed by standard recombinant methodology. Cells
CC expressing H4 receptor protein at a detectable level can suppress cyclic
CC adenosine monophosphate (cAMP) formation when contacted with the H4
CC receptor agonist. The H4 receptor and antibodies are used for identifying
CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
CC for treating transplanted organ rejection, asthma, allergies and
CC autoimmune pathologies such as multiple sclerosis, type 1 diabetes,
CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
CC protein and nucleic acids are useful targets to identify drugs that are
CC effective in treating disorders associated with histamine-regulated
CC processes. Identification and isolation of H4 receptor provides for
CC development of screening of molecules that interact with H4 receptors.
CC Genetic variants of H4 can be used to diagnose an H4 associated disease
CC as described above. The H4 receptor polynucleotide is useful to treat or
CC prevent a disorder associated with the function of H4 in peripheral blood
CC leukocytes. The present sequence represents the human histamine H4
CC receptor protein
XX
SQ Sequence 390 AA;
```

```
Query Match 66.9%; Score 1370.5; DB 5; Length 390;
Best Local Similarity 68.1%; Pred. No. 2.1e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSFPAFAIMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
1 MPDTNSTINLSLSTRVTLAFMSLVAFALMGNALVILAFVVDKRLHRSSYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVSNV 120
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYVNLISYDRYLSVSNV 120
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLIASDSWKNSTNTKDCBPGFVTEWYILIT 180
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
121 SYRTQHTGVLKIVTLMAVAVILAFVNGPMLLVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLLEFLLPVISVAYENVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
179 SFLEFVIPVILVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSITAFKVGFSWSESAAALQREYAEALLRG 300
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
239 SASTEPVASFHSEQRQRKSSLMFSSRTVMNSITASKMGFSQSDSVVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSVNPFLY 360
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
299 RRLAKSLAILLGVAFVCAWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQFNFSVNPFLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 391
Db |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
359 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 390
```

```
RESULT 13
AAU74906
ID AAU74906 standard; protein; 390 AA.
XX
XX AAU74906;
XX
XX 09-APR-2002 (first entry)
```

XX DE Amino acid sequence of human G-protein coupled receptor TGR62 protein.

XX Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease;

KW signal transduction modulator; cerebral cavernous malformation;

KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;

KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;

KW spleen-associated disorder; immune disorder.

XX OS Homo sapiens.

XX WO200200719-A2.

XX 03-JAN-2002.

XX 25-JUN-2001; 2001WO-US020363.

XX 23-JUN-2000; 2000US-0213461P.

XX (TULA-) TULARIK INC.

XX Lin DC, Zhao J, Chen J, Cutler G;

XX WPI; 2002-147880/19.

XX N-PSDB; ABK12959.

XX New G-protein coupled receptor polypeptides, useful for identifying

PT modulators of signal transduction for treating kidney disease,

PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.

XX Claim 26; Page 61; 78pp; English.

XX The present invention relates to a new G-protein coupled receptor (GPCR)

CC polypeptide comprising greater than 70% amino acid sequence identity to

CC the amino acid sequence of human GPCRs TGR62, TGR130.1, TGR130.2,

CC human TGR130.2, 80% amino acid sequence identity to mouse TGR18 or

CC 90% amino acid sequence identity to human novel edg receptor protein, as

CC defined in the specification. The GPCR covalently linked to a solid phase

CC is useful for identifying a compound that modulates signal transduction.

CC The identified compounds are useful for treating kidney disease, cerebral

CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac

CC myxoma. The molecules of the invention are useful for diagnosing

CC disorders or conditions such as kidney-related conditions or diseases

CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic

CC urinary abnormalities, renal tubule defects, hypertension and

CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,

CC infiltrations, lesions, functional disorders and jaundice and spleen-

CC associated disorders or conditions e.g. splenic enlargement, immune

CC disorders, blood disorders and others. Modulation of the polypeptide of

CC the invention is useful to treat or prevent any of the above conditions

CC or diseases. The present amino acid sequence represents the human GPCR

CC TGR62 protein of the invention. This sequence is one of seven novel G

CC protein coupled receptors of the invention (AAU74904- AAU74911)

XX Sequence 390 AA;

SQ

Query Match 66.9%; Score 1370.5; DB 5; Length 390;

Best Local Similarity 68.1%; Pred. No. 2.1e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMLSSPAFAIMGVNAVILAFVVDRLRHRSNYFFNLAI 60

DB 1 MPDTNSTINLSLSTRVTLFAFFMSLVAFALMLGNALVILAFVVDKRLRHRSNYFFNLAI 60

QY 61 DFLVGLISIPYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIIVLISYDRYSVNAV 120

DB 61 DFFVGVISIPYIPHTLFEWDFGKEICVFELTDTLLCTASVYNIIVLISYDRYSVNAV 120

QY 121 SYRAOHTGIMKVAQWVAVILAFVNGPMILASDSWKNTNTKDCPEGFVTEWYLTIT 180

DB 121 SYRTQHTGIVKIVTLVAVVAVILAFVNGPMILVSESKDEGS--EECEGFVSEWYLTIT 178

QY 181 MLLEFLLPVISVAYFNVQIYVLSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACRTSN 240

Db 179 SFLEFVIPVILVAYFNNIYVLSLWKRRDLHSLRCOSHPGLTAVSSNICHSFGRUSRRSL 238

QY 241 PGLKESASRHSRSPREKSSILVSLRTHMNSSITAFKVGSRFMRSESAALRQREYAEILRG 300

Db 239 SASTEVPAFSEQRKSSLMFSSRTYKMSNTTASKMGFSQSDSVALLHQREHVELLRA 298

QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360

Db 299 RRLAKSLAILLGFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFLQWNSFVNPLY 358

QY 361 PLCHRRFQKAPFWKILCVTKWPAISQ-NQSVSS 391

Db 359 PLCHRRFQKAPFLKIFCIKKQPLPSQHGSRVSS 390

RESULT 14

ABG71960

ID ABG71960 standard; protein; 390 AA.

XX AC ABG71960;

XX 28-JAN-2003 (first entry)

XX Human G-protein coupled receptor AXOR35.

XX Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte;

KW macrophage; eosinophil; neutrophil; infection; transplant rejection;

KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;

KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;

KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;

KW psoriasis; urological disease; urinary retention; cardiovascular disease;

KW myocardial infarction; hypotension; hypertension; pulmonary disorder;

KW chronic obstructive pulmonary disease; cough; renal disease;

KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosia;

KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;

KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;

XX graft versus host disease; osteoporosis.

XX Homo sapiens.

XX US2002137054-A1.

XX 26-SEP-2002.

XX 20-JUL-2001; 2001US-00910411.

XX 02-NOV-1999; 99US-00431898.

XX 03-FEB-2000; 2000US-00497790.

XX 20-OCT-2000; 2000US-00693761.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;

PI Michalovich D, Morrow DM, Zhu Y;

XX WPI; 2003-074982/07.

DR N-PSDB; ABS57063.

XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for

PT treating infections, gastrointestinal disorders, autoimmune disorders,

PT urological diseases, cardiovascular diseases and cancer.

XX Claim 1; Page 22; 24pp; English.

CC The invention relates to an isolated G-protein coupled receptor

CC polypeptide, AXOR35, (and its homologues and variants) and its encoding

CC polynucleotide (and its homologues, variants, complements and RNA

CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35

CC expression vector, producing a recombinant host cell by introducing the

CC vector into a cell, such that the host cell produces AXOR35, a membrane of

CC the host cell expressing AXOR35, identifying/screening for agonists or

CC antagonists of AXOR35 and inhibiting or promoting the function of
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,
 CC by administering to the patient AXOR35 agonists or antagonists. The
 CC agonist or antagonist identified is useful for treating a disease such as
 CC asthma, or for inhibiting or promoting the function of lymphocytes,
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,
 CC for identifying compounds that are agonists or antagonists of AXOR35, as
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or
 CC viral infections), transplant rejection, gastrointestinal disorders (such
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
 CC psoriasis), neurological diseases (such as urinary retention),
 CC cardiovascular diseases (such as myocardial infarction), hypotension,
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary
 CC disease), cough, renal diseases (such as renal ischaemia),
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
 CC versus host disease and osteoporosis. The present sequence represents
 CC human AXOR35
 XX
 SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 6; Length 390;
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
 QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVDRNLHRNSYFFLNLAIS 60
 Db 1 MPTDNTINLSLSTRVTLAFAFMSLVAFALMGNALVILAFVDRNLHRNSYFFLNLAIS 60
 QY 61 DFLVGLISPIYIPHYLVFNWFGSGICMFWLTIDYLLCTASVYNIVLISYDRYQSVNAV 120
 Db 61 DFFVGVISPIYIPHYLVFNWFGSGICMFWLTIDYLLCTASVYNIVLISYDRYQSVNAV 120
 QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDWSKNSNTKDCPPGVTEWYIITIT 180
 Db 121 SYRQHTGVKLIVLMVAVWVILAFVNGPMLVSESKDGS--ECEPGFFSEWYIIT 178
 QY 181 MLEFLLPVTISVAVENVOIYWSLWKRALSRCSHPAGFTSTSSAGSHLRAGVARTSN 240
 Db 179 SFLEFVPIVILYAFNNIYWSLWKRDHLRSCQSHPLGTAVSSNICCHSPGRSLSRSL 238
 QY 241 PGLKESAAHRHSPSRKSSILVSLTHMNSSITAFKGVSWFSESAAALRQRYAELLRC 300
 Db 239 SASTVPASFHSEQRQRKSLMFSSTTKMNSNTIASKMGFSOSDVALHQREHVELLRA 298
 QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPPFLY 360
 Db 299 RRLAKSLAILLGVAVCWAPYSLEFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPPFLY 358
 QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391
 Db 359 PLCHRRFQKAFKIFCIKQPLFSQHSRVS 390

RESULT 15
 ABU92265
 ID ABU92265 standard; protein; 390 AA.
 XX
 AC ABU92265;
 XX
 DT 16-JUL-2003 (first entry)
 XX
 DE Human G protein-coupled receptor hrup7.
 XX
 KW Human; receptor; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
 KW hARE-5; hrup3; hrup5; hrup6; hrup7; hgPCR27; hARE-1; hARE-2; hPR1; hg2A;
 KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hrup4; signalling cascade.
 XX
 OS Homo sapiens.

XX
 EN US2003017528-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 06-JUN-2001; 2001US-00875076.
 XX
 PR 20-NOV-1998; 98US-0109213P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0136567P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 28-SEP-1999; 99US-0156333P.
 PR 29-SEP-1999; 99US-0156555P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 12-OCT-1999; 99US-00417044.
 XX
 PA (CHEN/) CHEN R.
 PA (DANG/) DANG H T.
 PA (LIAN/) LIAN C W.
 PA (LINI/) LIN I.
 XX
 PI Chen R, Dang HT, Liaw CW, Lin I;
 XX
 XX WPI: 2003-428952/40.
 DR N-PSDB; ACA93282.
 DR
 XX Novel endogenous, orphan, human G protein-coupled receptors useful for
 PT identification of modulators of the receptor and as research tools for
 PT understanding the role of the receptor in human body.
 PT
 XX Claim 26; Page 23; 54pp; English.
 PS
 XX The invention relates to a human G protein-coupled receptor (GPCR)
 CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
 CC hARE-3, hARE-4, hARE-5, hrup3, hrup5, hrup6, hrup7, hgPCR27, hARE-1, hARE
 CC -2, hPR1, hg2A, hCHN3, hCHN4, hCHN6, hCHN9, hCHN10 and hrup4.
 CC Also included are a plasmid comprising a vector and one of the cDNAs
 CC above and a host cell comprising the plasmid. The GPCRs are useful for
 CC the direct identification of candidate compounds as inverse agonists,
 CC agonists or partial agonists. In vitro and in vivo systems incorporating
 CC GPCRs is useful for elucidating and understanding the roles these
 CC receptors play in the human condition, both normal and diseased, as well
 CC as understanding the role of constitutive activation as it applies to
 CC understanding the signalling cascade. The cDNAs are useful for making a
 CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR
 CC identification of the expression of the receptor in tissue samples. The
 CC present sequence represents a GPCR of the invention
 XX
 SQ Sequence 390 AA;
 Query Match 66.9%; Score 1370.5; DB 6; Length 390;
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
 QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVDRNLHRNSYFFLNLAIS 60
 Db 1 MPTDNTINLSLSTRVTLAFAFMSLVAFALMGNALVILAFVDRNLHRNSYFFLNLAIS 60
 QY 61 DFLVGLISPIYIPHYLVFNWFGSGICMFWLTIDYLLCTASVYNIVLISYDRYQSVNAV 120
 Db 61 DFFVGVISPIYIPHYLVFNWFGSGICMFWLTIDYLLCTASVYNIVLISYDRYQSVNAV 120
 QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDWSKNSNTKDCPPGVTEWYIITIT 180
 Db 121 SYRQHTGVKLIVLMVAVWVILAFVNGPMLVSESKDGS--ECEPGFFSEWYIIT 178

QY	181	MLLEFLLPVISVAYFNQIYWSLWKRALSRCPHAGFSTTSSASGHLHRAGVACRTSN	240
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Db	239	SASTEVPASPHSERQRRKSSILMFSSRTKMNSNTIASKMGSEFSQSDSVALHQREHVELLRA	298
QY	301	RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY	360
Db	299	RRLAKSLAILLGVEAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLY	358
QY	361	PLCHRRRQKAFWKILCVTKWPAISO-NOSVSS	391
Db	359	PLCHRRRQKAFWKILCVTKWPAISO-NOSVSS	390

Search completed: October 1, 2004, 10:11:32
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:10:33 ; Search time 18 Seconds
(without alignments)
1121.431 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAISQNSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1370.5	66.9	390	3	US-09-414-010-2
2	1370.5	66.9	390	4	US-09-812-216-2
3	722.5	35.3	445	2	US-08-985-090-2
4	722.5	35.3	445	3	US-09-165-543-2
5	722.5	35.3	445	3	US-09-167-354-7
6	722.5	35.3	445	4	US-09-642-853-7
7	722.5	35.3	445	4	US-09-642-514-7
8	716.5	35.0	445	3	US-09-165-543-5
9	621.5	30.3	351	4	US-09-524-162-2
10	582.5	28.4	362	2	US-08-985-090-5
11	582.5	28.4	362	3	US-09-165-543-32
12	427	20.8	348	4	US-08-118-270-13
13	427	20.8	348	5	PCT-US93-08528-13
14	427	20.8	355	1	US-08-118-270-11
15	427	20.8	355	5	PCT-US93-08528-11
16	415.5	20.3	479	3	US-08-313-553-7
17	415.5	20.3	479	3	US-08-767-993-7
18	393	19.2	354	3	US-08-313-553-9
19	393	19.2	354	3	US-08-767-993-9
20	390.5	19.1	501	1	US-08-722-001-14
21	390.5	19.1	501	2	US-08-467-568-9
22	390.5	19.1	501	2	US-09-030-582-9
23	389.5	19.0	513	3	US-08-406-855A-21
24	389.5	19.0	513	3	US-09-206-899-21
25	389.5	19.0	515	1	US-08-444-734A-7
26	389.5	19.0	515	2	US-08-406-855A-22
27	389.5	19.0	515	3	US-09-206-899-22

28	388.5	19.0	572	1	US-08-334-698-2	Sequence 2, Appli
29	388.5	19.0	572	1	US-08-328-932-2	Sequence 2, Appli
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32	388.5	19.0	572	2	US-08-406-855A-2	Sequence 2, Appli
33	388.5	19.0	572	2	US-08-722-190-2	Sequence 2, Appli
34	388.5	19.0	572	3	US-08-244-354-2	Sequence 2, Appli
35	388.5	19.0	572	3	US-09-206-899-2	Sequence 2, Appli
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37	388.5	19.0	572	4	US-09-688-415-2	Sequence 2, Appli
38	388.5	19.0	572	4	US-09-444-783-2	Sequence 2, Appli
39	388.5	19.0	572	5	PCT-US95-04203-2	Sequence 2, Appli
40	387.5	18.9	515	4	US-09-688-415-9	Sequence 9, Appli
41	386.5	18.9	515	1	US-08-722-001-25	Sequence 25, Appli
42	385.5	18.8	515	3	US-09-032-742-5	Sequence 5, Appli
43	385.5	18.8	515	4	US-09-688-415-10	Sequence 10, Appli
44	385	18.8	559	2	US-08-406-855A-20	Sequence 20, Appli
45	385	18.8	559	3	US-09-206-899-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Omland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2

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Best Local Similarity	68.1%	Pred. No.	7.2e-106				
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Gaps	2						
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Db	1	MDTNTSTINLSLSTRVTTLAFMSLVAFALMGNALVILAFVVDKXLRHRSYFFLNLAIS	60				
QY	61	DFVLGLISIPYIPHLVFNWFGSICFWLITDYLLCTASVINVLISYDRASVSNV	120				
Db	61	DFVGVISIPYIPHLVFNWFGSICFWLITDYLLCTASVINVLISYDRASVSNV	120				
QY	121	SYRAQHTGIMKIVAOQVAVILAFVNGPMLASDKWNTKDCPEGVTEWILAIT	180				
Db	121	SYRQHTGVILVILMAVAVLAFVNGPMLVSVESWDEGS--ECEPGFFSEWILAIT	178				
QY	181	MLLEFLLPVIIVAVFNQIYWSLMKRRALRCPHAGFTTSSASGHLHAGVACRTSN	240				
Db	179	SFLEFVIVILVAVFNQIYWSLMKRDHLRCQSHPGTLAVSSNICGHSFRGLSSRSL	238				
QY	241	PGLKESARSRHSEPRKXSSILVSLRTHMSSITAFKVGSWRSESAALROREVAELRG	300				
Db	239	SASTVEPASFHSEQRKXSSLMFSRTKMNSTIASKMGFSQSDSVLHOREHVELRA	298				
QY	301	RKLARSLLAISAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWENSFWNP	360				

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Db 359 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 390
RESULT 2
US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monisma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812.216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2
Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 7.2e-106;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNLRHRSNYFFNLNLAIS 60
Db 1 MPDNTNINLSLSTRTVLAFFMSLVAFAMVGNVILAFVVDNLRHRSNYFFNLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLISYDRYOSVNAV 120
Db 61 DFFGVISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLISYDRYOSVNAV 120
QY 121 SYRAQHTGIMKIVAQWAVILAFVNGPMILASDSWKNSTNTKDCPCGFTVETWILIT 180
Db 121 SYRTQHTGVKIVTLMAVAVILAFVNGPMILASDSWKNSTNTKDCPCGFTVETWILIT 178
QY 181 MLLEFLLPVIVAVENVOIYVSLMKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAVENVOIYVSLMKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 238
QY 241 PGLKESAAHSESPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAFSEHQRKRSKSLMFSRTKMSNTIASKGFSQSDVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYRIAFWLQWFNQFVNPLLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNQFVNPLLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 391
Db 359 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 390
RESULT 3
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-2
Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 4e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;
QY 18 LAFUWSSGFAFAMVGNVILAFVVDNLRHRSNYFFNLNLAISDFLVGLISIPLYIPHLV 77
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Db 157 LLVWVLAFLYGPAIL-----SWEYLGGSSIPEGHCYAEFFYNWYFLITASTLEFTTFLS 213
QY 192 VAVENVOIY-----WSLWKRRLSRCPSH 215
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QY 216 -----AGFTSTSSASGHLHRAGVACRTSNPGLKESAAHSESPRRKSSILV 263
Db 274 RYGVGEAAVGAAGEATLGGGGG-----GSVASPTSSSG-----SSRGTETPR----- 318
QY 264 SLRTHMNSSITAFKVGSEFWRSESAALRQ-----EYAEFLRGRKLARSLAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKNVQSFTQRFSLDRDKVAKSLAVIVSIF 367
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Db 427 LCPQK 431
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US-09-165-543-2

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNQFVNPLLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 391
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RESULT 2
US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monisma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812.216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2
Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 7.2e-106;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNLRHRSNYFFNLNLAIS 60
Db 1 MPDNTNINLSLSTRTVLAFFMSLVAFAMVGNVILAFVVDNLRHRSNYFFNLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLISYDRYOSVNAV 120
Db 61 DFFGVISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLISYDRYOSVNAV 120
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Db 121 SYRTQHTGVKIVTLMAVAVILAFVNGPMILASDSWKNSTNTKDCPCGFTVETWILIT 178
QY 181 MLLEFLLPVIVAVENVOIYVSLMKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAVENVOIYVSLMKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 238
QY 241 PGLKESAAHSESPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAFSEHQRKRSKSLMFSRTKMSNTIASKGFSQSDVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYRIAFWLQWFNQFVNPLLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNQFVNPLLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 391
Db 359 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 390
RESULT 3
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

```

Db      427 LCPQK 431
|| |
RESULT 5
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Brandler, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-167-354-7

Query Match          35.3%; Score 722.5; DB 3; Length 445;
Best Local Similarity 38.8%; Pred.No. 4e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY   18 LAFLMSSFAFALMVGNAAVILAFVVDNLRHRSNYFFLNLAISDFLYCLGISIPLYIPIHL 77
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   37 LAALMALLIIVATVLGNALVWMLAFVADSSLTKQNFFLLNLAISDFLVGAFICPLYPVPYL 96
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSRAOHTGIMKIYAQM 136
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   97 TGRMTFGRGLCKLWLVDYLLCTSSAFNVILISYDRFLSVTRAVSYAQOGDTRAVRKM 156
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   137 VAWVILAFLVNGPMILASDSWK-----NSTNTKDCBPGFTVEWILTITMLLEFLLPVIS 191
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLTITASTLEFFTPLFS 213
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   192 VAYFNVOIY-----NSLKWRALSRCPSH 215
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   214 VTFFNLSIYNIQRTEFLRLDGAREAGPEPPPEAPQSPPPPCCGCWGKGHGHEAMPLH 273
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   216 -----AGFTTSSASGHILHRAGVACRTNPGLKESAASRHSPPRKSSILV 263
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   274 RYGVGEEAAGAAGEATLGCGGGG---GSVASPTSSG----SSRGTERPR----- 318
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   264 SLRTHNSSITAFKVCSFWKSESAAALRQR-----EVAELLRRGKLARSLAILLSAF 314
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   319 -----SLKRSGKSPSASSASLEKRMKWVSQSFTQRFRLSRDKVKAKSLAVIVSF 367
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   315 AICWAPYCLFTIVLSTYPTERPKSWYSYTAFWLQNFNSFVNPFYPLCHRRFRQKAFWKI 374
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB   368 GLCWAPYTLLMIIRAACHGVCP-DIWYETSFLLWANGAVNEVLYPLCHHSFRRAFTKL 426
    ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY   375 LCVTK 379
    |||
DB   427 LCPQK 431

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```
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-855-7

Query Match          35.3%; Score 722.5; DB 4; Length 445;
Best Local Similarity 38.8%; Pred. No. 4e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY      18 LAFMSSFAFMVGNNAVILAFVDNRNLRHSNYFFLNLAISDFVLGLTSLPIYLPHVL 77
       ||| :||:||||| |:||:|:|:||||| |:||:|:|:||||| |:||:|:|:|||||
Db      37 LAALMALLIIVATVLGNALVMFLAFVADSSLRTQNFFLLNLTAISDFLVGAFCLIPLYVPVL 96

QY      78 F-NWNFGSGICMEWLIIDYLLCTASVYNIVLISYDRYOSVSNVSYRAQHTGIMKIVAQM 136
       ||| :||:||||| |:||:|:~|:||||| |:||:|:~|:||||| |:||:|:~|:|||||
Db      97 TGRWTTFGRGLCKMLVVDDYLLCTSSAFNVILISYDRFLSVTRAVSYRAQQDTRRAVRKM 156

QY      137 VAVWILAFLVNGPMILASDWK-----NSTMKDCPEGFVTWEWILITITMLEFLLPVIS 191
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      157 LLVWVLAFLLYGPAIL---SWEYLGGGSIPEGHCYAEEFFYNWYFLITASTLEFFTPLS 213

QY      192 VAYENVQIY-----WSLWKRRALSRCPSH 215
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      214 VTFFNLGIYLIQRIRLDGAREAGPEPPPAQSPPPPCCWGCGWQHGEAMPJH 273

QY      216 -----AGFTSTSSASGHLHRAGVACTNSPGLKESAAASHSESPRKRKSILV 263
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      274 RYGVEAAGVAEAGEANTLGCGGG---GSVASPTSSSG----SSSRGTETPR----- 318

QY      264 SLRTHMNSSITAFKVGSGFWRSESAALRQ-----EYAEILLRGKLASLAILLSAF 314
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      319 -----SLKRQKPSASSASLEKRMKVQSQTQRFLSDRKRVAKSLAVIVSIF 367

QY      315 AICWAPYCLFTIVLTSTPYRTERPKSVWYSIAFWLQWFNSFVNPFYLPCHRRFOKAFWKI 374
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      368 GLCWAPYTLMIIRAAACHGVCP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKL 426
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      375 LCVTK 379
       ||| :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      427 LCPQK 431

RESULT 7
US-09-642-514-7
; Sequence 7, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORTI290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
```

```
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-5

Query Match      35.0%; Score 716.5; DB 3; Length 445;
Best Local Similarity 40.2%; Pred. No. 1.3e-51;
Matches 165; Conservative 54; Mismatches 128; Indels 63; Gaps 10;

QY 18 LAFLMSSFAFALMGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVLGNALVLMFAFVADSSLRTONNFFLNLAISDFLVGAFICPLYVPYL 96

QY 78 F-NWNFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVSNVSYRAOHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYRAOQGDTRRVRKM 156

QY 137 VAVWILAFVNGPMLASDSWK-----NSTNTKDCPEGFVTEWYILITITMLLEFLPLVIS 191
Db 157 ALVWVLAFLLYGPAIL--SWEYLSGSGSIPEGHCVAFYFNWYFLITASTLEFFTFPLS 213

QY 192 VAVFNQIYWSLWKRRAL-----SRCPSHAGFTSTSSASGH-----LH 230
Db 214 VTFNLSIYLNIOQRTLRDLGGREGAPPPPPAPPPSCWCKGHEAMPLH 273

QY 231 RAGVACRTNPNGLK-----ESAASHSESPPRKSILVSLRTHM 269
Db 274 RYGVG--EAGPGVEAGEALGGSGGGAASPTSSGSSSRGTERPR-----SLKRG 324

QY 270 NSGITAFKVGSWFSESAALRQREYAEALLRGLKRLARSALILSAFAICWAPYCLFTIVLS 329
Db 325 KPSASASLEKMKMYSQSITOR--FRLSDKKVAKSLAIVSIFGLCWAPYTLMLIIRA 382

QY 330 TYPRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVTK 379
Db 383 ACHGRCP--DYWYETSFLLWANSVAVNPVLYPLCHYSFRRAFTKLLCPQK 431

RESULT 9
US-09-524-162-2
; Sequence 2, Application US/09524162
; Patent No. 6355452
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
; CURRENT APPLICATION NUMBER: US/09/524,162
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRP
; ORGANISM: HOMO SAPIENS
US-09-524-162-2

Query Match      30.3%; Score 621.5; DB 4; Length 351;
Best Local Similarity 38.3%; Pred. No. 7.1e-44;
Matches 141; Conservative 44; Mismatches 110; Indels 73; Gaps 8;

QY 18 LAFLMSSFAFALMGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVLGNALVLMFAFVADSSLRTONNFFLNLAISDFLVG----- 84

us-08-985-090-5
; Sequence 5, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-5

Query Match      28.4%; Score 582.5; DB 2; Length 362;
Best Local Similarity 37.7%; Pred. No. 1.3e-40;
Matches 137; Conservative 45; Mismatches 118; Indels 63; Gaps 10;

QY 65 GLISIPLYIPHLVLF-NWNFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVSNVSYR 123
Db 1 GAFICPLYVPVLTGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYR 60
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1 GAPCIPLYVPVLTGRWTFGRGLKWLVDYLLCASSVFNILISYDRFLSVTRAVSYR 60
124 AQTGIMKIQAQVAVWILAFVNGPMILASDWSK-----NSTNTKDCBPGFVTEWYILT 178
61 AQOQDTRRAVRKMAVWVLAFLYGPAIL---SWEYLSGGSSIPGEGHCYAEFFYNWYFLI 117
179 ITMLBFLPLVISVAVFNVOIYWSLWKRRAL-----SRCPSHAGFSTTS 222
118 SASLLEFFTFPLSVTFENLSIYLNIOQRTRLRDGGREGAPPPDPAQPPPPAPPSCWG 177
223 SSASGH-----LHRAGVACRTSNPGLK-----ESAASHSESPR 256
178 CWPKGHEAMPLHRYGVG--EAGPGVEAGEAALGGSGGGAASPTSSSGSSRGTERPR 235
257 RKSSILVSLRTHMNSSITAFKVGSWFSESAALRQREYAEILLRGRKLARSAILLSAFAI 316
236 -----SLKRGKSPSASSASLEKRMKMWQSITQR--FRLSRDKKVAKSLAIVSIFGL 286
317 CWAPYCLFTIVLSTYPTERPCKSVWYSIAFWLWNSFVNPFLYPLCHRRFPQKAFWKILC 376
287 CWAPYTLMLIRACHGRCIP-DYWYETSFLLWANSVNPVLPVPLCHYSFRRAFTKLLC 345
377 VTK 379
346 PQK 348

RESULT 12
US-08-118-270-13
; Sequence 13, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-13

124 AQTGIMKIQAQVAVWILAFVNGPMILASDWSK-----NSTNTKDCBPGFVTEWYILT 178
61 AQOQDTRRAVRKMAVWVLAFLYGPAIL---SWEYLSGGSSIPGEGHCYAEFFYNWYFLI 117
179 ITMLBFLPLVISVAVFNVOIYWSLWKRRAL-----SRCPSHAGFSTTS 222
118 SASLLEFFTFPLSVTFENLSIYLNIOQRTRLRDGGREGAPPPDPAQPPPPAPPSCWG 177
223 SSASGH-----LHRAGVACRTSNPGLK-----ESAASHSESPR 256
178 CWPKGHEAMPLHRYGVG--EAGPGVEAGEAALGGSGGGAASPTSSSGSSRGTERPR 235
257 RKSSILVSLRTHMNSSITAFKVGSWFSESAALRQREYAEILLRGRKLARSAILLSAFAI 316
236 -----SLKRGKSPSASSASLEKRMKMWQSITQR--FRLSRDKKVAKSLAIVSIFGL 286
317 CWAPYCLFTIVLSTYPTERPCKSVWYSIAFWLWNSFVNPFLYPLCHRRFPQKAFWKILC 376
287 CWAPYTLMLIRACHGRCIP-DYWYETSFLLWANSVNPVLPVPLCHYSFRRAFTKLLC 345
377 VTK 379
346 PQK 348

RESULT 11
US-09-165-543-32
; Sequence 32, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-32
Query Match 28.4%; Score 582.5; DB 3; Length 362;
Best Local Similarity 37.7%; Pred. No. 1.3e-40;
Matches 137; Conservative 45; Mismatches 118; Indels 63; Gaps 10;
65 GLISIPLYIPHVLF-NWNFGSGICMFWLITDYLCTASVYNVILISYDRYQSVNAVSYR 123

TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-11

Query Match 20.8%; Score 427; DB 5; Length 355;
Best Local Similarity 29.6%; Pred. No. 9.3e-28;
Matches 110; Conservative 75; Mismatches 123; Indels 64; Gaps 13;

QY 18 LAFIMSSFAFAMVGNVAVILAFVDRNLHRNRYFFNLAIISDFLVGLISIPLYIPIHVL 77
Db 3 IAFETGILAVTIIGNLIVVFKVKKQLKTVNNYFLLSLACADLIIGVISMNLFTTYII 62
QY 78 FN-WNFGSGICMFWLITDYLLCTASVYVNIIVISYDRYQSVNAVSYRAQHT----GIMKI 132
Db 63 MNRWALGNTACDLWIAIDYVNASVNLNLLVISFDRYFSITRPLTYRAKRTTKRAGVMIG 122
QY 133 VAQWAVWILAFVNGPMILASDSKNSNTKCEPG-----FVTEWVILITMLLEFLL 187
Db 123 LA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFIQFUSEPTITFGTAIAAFYM 174
QY 188 PVISVAYFNVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN----PGL 243
Db 175 PVIMRI-----LYWRIYKETE-KTKELAG-----LQASGTEAETENFVHPTGS 218
QY 244 KESAAASHSPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEALLRGRKL 303
Db 219 SRSCSSVELQOKR-----FALKT--RSQITKRKL-----LVKEKKA 253
QY 304 ARSLAILLSAFAICWADYCLFTIVLSTYPRTERPKSVWYSTAFWLOWNSFVNPFLYPLC 363
Db 254 AQTLSAILLAFIITWTPTNIMVLV-NTFCDSICPKTYWNLGGYWLVCYINSTVNPVCYALC 312
QY 364 HRRFOKAFWKIL 375
Db 313 NKTFRTFKILL 324

Search completed: October 1, 2004, 10:13:27
Job time : 20 secs

SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-11

Query Match 20.8%; Score 427; DB 1; Length 355;
Best Local Similarity 29.6%; Pred. No. 9.3e-28;
Matches 110; Conservative 75; Mismatches 123; Indels 64; Gaps 13;

QY 18 LAFIMSSFAFAMVGNVAVILAFVDRNLHRNRYFFNLAIISDFLVGLISIPLYIPIHVL 77
Db 3 IAFETGILAVTIIGNLIVVFKVKKQLKTVNNYFLLSLACADLIIGVISMNLFTTYII 62
QY 78 FN-WNFGSGICMFWLITDYLLCTASVYVNIIVISYDRYQSVNAVSYRAQHT----GIMKI 132
Db 63 MNRWALGNTACDLWIAIDYVNASVNLNLLVISFDRYFSITRPLTYRAKRTTKRAGVMIG 122
QY 133 VAQWAVWILAFVNGPMILASDSKNSNTKCEPG-----FVTEWVILITMLLEFLL 187
Db 123 LA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFIQFUSEPTITFGTAIAAFYM 174
QY 188 PVISVAYFNVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN----PGL 243
Db 175 PVIMRI-----LYWRIYKETE-KTKELAG-----LQASGTEAETENFVHPTGS 218
QY 244 KESAAASHSPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEALLRGRKL 303
Db 219 SRSCSSVELQOKR-----FALKT--RSQITKRKL-----LVKEKKA 253
QY 304 ARSLAILLSAFAICWADYCLFTIVLSTYPRTERPKSVWYSTAFWLOWNSFVNPFLYPLC 363
Db 254 AQTLSAILLAFIITWTPTNIMVLV-NTFCDSICPKTYWNLGGYWLVCYINSTVNPVCYALC 312
QY 364 HRRFOKAFWKIL 375
Db 313 NKTFRTFKILL 324

RESULT 15
PCT-US93-08528-11
Sequence 11, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:11:54 ; Search time 134 Seconds
(without alignments)

938.981 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKPALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1370.5	66.9	390	10	US-09-852-165-2
3	1370.5	66.9	390	10	US-09-891-138A-6
4	1370.5	66.9	390	12	US-10-349-253A-2
5	1370.5	66.9	390	12	US-09-875-076-14
6	1370.5	66.9	390	12	US-09-876-252-14
7	1370.5	66.9	390	13	US-10-052-193-2
8	1370.5	66.9	390	14	US-10-225-567A-629
9	1370.5	66.9	390	14	US-10-272-983-14
10	1370.5	66.9	390	14	US-10-354-769-2
11	1370.5	66.9	390	14	US-10-393-807-14
12	1370.5	66.9	390	15	US-10-417-820A-14
13	1370.5	66.9	390	16	US-10-696-673-2
14	1370.5	66.9	390	16	US-10-723-955-14
15	1370.5	66.9	390	16	US-10-737-619-2

16	1370.5	66.9	390	16	US-10-782-596-14	Sequence 14, Appl
17	1366.5	66.7	390	14	US-10-290-078-27	Sequence 27, Appl
18	722.5	35.3	445	9	US-09-350-206-2	Sequence 2, Appl
19	722.5	35.3	445	9	US-09-349-755-2	Sequence 2, Appl
20	722.5	35.3	445	9	US-09-166-334-2	Sequence 2, Appl
21	722.5	35.3	445	14	US-10-282-958-2	Sequence 2, Appl
22	722.5	35.3	445	14	US-10-225-567A-549	Sequence 549, App
23	722.5	35.3	445	16	US-10-453-106-1	Sequence 1, Appl
24	722.5	35.3	445	16	US-10-727-021-7	Sequence 7, Appl
25	722.5	35.3	445	12	US-09-891-053-20	Sequence 20, Appl
26	718.5	35.1	445	16	US-10-453-106-2	Sequence 2, Appl
27	716.5	35.0	445	9	US-09-350-206-5	Sequence 5, Appl
28	716.5	35.0	445	9	US-09-349-755-5	Sequence 5, Appl
29	716.5	35.0	445	9	US-09-166-334-5	Sequence 5, Appl
30	716.5	35.0	445	12	US-09-891-053-25	Sequence 25, Appl
31	716.5	35.0	445	14	US-10-282-958-5	Sequence 5, Appl
32	716.5	35.0	445	16	US-10-453-106-3	Sequence 3, Appl
33	709.5	34.6	413	12	US-09-891-053-1	Sequence 1, Appl
34	591	28.9	441	16	US-10-398-036-3	Sequence 3, Appl
35	582.5	28.4	362	9	US-09-350-206-32	Sequence 32, Appl
36	582.5	28.4	362	9	US-09-349-755-32	Sequence 32, Appl
37	582.5	28.4	362	9	US-09-166-334-32	Sequence 32, Appl
38	582.5	28.4	362	14	US-10-282-958-32	Sequence 32, Appl
39	413	20.2	460	14	US-10-225-567A-188	Sequence 188, App
40	413	20.2	478	13	US-10-029-009-10	Sequence 10, Appl
41	413	20.2	498	13	US-10-029-009-22	Sequence 22, Appl
42	410	20.0	460	9	US-09-782-980-82	Sequence 82, Appl
43	410	20.0	460	9	US-09-884-430-6	Sequence 6, Appl
44	410	20.0	460	12	US-10-423-543-93	Sequence 93, Appl
45	410	20.0	460	14	US-10-336-489-6	Sequence 6, Appl

ALIGNMENTS

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RESULT 1
US-09-910-411-2
; Sequence 2: Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

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Query Match 66.9%; Score 1370.5; DB 9; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSENSTGILPPAAQVPLAFMSFAIMVGNVILAFVVDNRHRSYFFFLNLAIS 60
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Db 1 MFDNSTINLSLSTRTVTLAFMSLVAFALGNALVILAFVVDNRHRSYFFFLNLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 DELVGLISIPLYIPIHVLENWNNFGSGICMFWLITDYLTASVYIVLISYDRYOSVGNV 120
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Db 61 DFFVGVISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120
QY 121 SYRAQHTGIMKIVAOVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVFTWYILTT 180
Db 121 SYRTQHTGVKIVTLVAVVWVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYVWLSWKRRLSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAYFNNIYVWLSWKRDLHLSRCQSHPLGTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWRSESAALRQREYAEILRG 300
Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY 360
Db 299 RRLAKSLAILLGFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO--NQSVSS 391
Db 359 PLCHKRFQKAFKIFCIKQKPLPSQHSRSVSS 390

RESULT 2

US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US2003032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US2003032784A1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231regUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

Query Match 66.9%; Score 1370.5; DB 10; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSESNTGILPPAAQVPLAFMSSPFAIMVGNVAVILAFVVDNRNLHRSNYFFLNLAIS 60
Db 1 MPDNTNSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDNRNLHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120
QY 121 SYRAQHTGIMKIVAOVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVFTWYILTT 180
Db 121 SYRTQHTGVKIVTLVAVVWVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYVWLSWKRRLSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAYFNNIYVWLSWKRDLHLSRCQSHPLGTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWRSESAALRQREYAEILRG 300
Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY 360
Db 299 RRLAKSLAILLGFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPALSO--NQSVSS 391
Db 359 PLCHKRFQKAFKIFCIKQKPLPSQHSRSVSS 390
RESULT 3
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1alel Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match 66.9%; Score 1370.5; DB 10; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
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Db 1 MPDNTNSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDNRNLHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120
QY 121 SYRAQHTGIMKIVAOVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVFTWYILTT 180
Db 121 SYRTQHTGVKIVTLVAVVWVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYVWLSWKRRLSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAYFNNIYVWLSWKRDLHLSRCQSHPLGTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWRSESAALRQREYAEILRG 300
Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY 360
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RESULT 4

US-10-349-253A-2
; Sequence 2, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura

APPLICANT: Graybill, Todd
APPLICANT: Li, Xiatong
APPLICANT: Michalovich, David
APPLICANT: Morrow, Dwight
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: ACR35, A G-Protein Coupled Receptor
FILE REFERENCE: GPT0655-2C2
CURRENT APPLICATION NUMBER: US/10/349,253A
PRIORITY FILING DATE: 2003-01-21
PRIORITY FILING DATE: 09/910,411
PRIORITY FILING DATE: 2001-07-20
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 09/693,761
PRIORITY FILING DATE: 2000-02-03
PRIORITY FILING DATE: 09/431,898
PRIORITY FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
US-10-349-253A-2

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Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

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DB 1 MPTDNTNLSLSTRVTLAFMSLVAFALMGNALVILAFVVDNRNLRHSNYFFNLALS 60
QY 61 DFLVGLISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120
DB 61 DFPVGVISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVQAVVAVVILAFVNGPMLASDWSKNSNTKDCPEGFVTEWYIIT 180
DB 121 SYRQHTGVLKIVLTVAVVAVVILAFVNGPMLVSESKDEGS--ECEPGFFSEWYIIT 178
QY 181 MLLEFLLPVISVAVYVNVQIYWSLWKRRLSRCPHAGFSTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIVPILVAFNNIYWSLWKRDLHRCQHPGLTAVSSNICGHSFGRLSRSL 238
QY 241 PGLKESAAHRHSESPRRKSSILVLRTHMNSSITAFKVGSEFWSAESALRQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFACWAPYCLFTTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLGFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391
DB 359 PLCHRRFQKAFKIFCIKKQPLPSQHSRVS 390

RESULT 5

US-09-875-076-14
Sequence 14, Application US/09875076
Publication No. US20030017528A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIORITY FILING DATE: 09/417,044
PRIORITY FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
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PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
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PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 66.9%; Score 1370.5; DB 12; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRNLRHSNYFFNLALS 60
DB 1 MPTDNTNLSLSTRVTLAFMSLVAFALMGNALVILAFVVDNRNLRHSNYFFNLALS 60
QY 61 DFLVGLISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120
DB 61 DFPVGVISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVQAVVAVVILAFVNGPMLASDWSKNSNTKDCPEGFVTEWYIIT 180
DB 121 SYRQHTGVLKIVLTVAVVAVVILAFVNGPMLVSESKDEGS--ECEPGFFSEWYIIT 178
QY 181 MLLEFLLPVISVAVYVNVQIYWSLWKRRLSRCPHAGFSTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIVPILVAFNNIYWSLWKRDLHRCQHPGLTAVSSNICGHSFGRLSRSL 238
QY 241 PGLKESAAHRHSESPRRKSSILVLRTHMNSSITAFKVGSEFWSAESALRQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFACWAPYCLFTTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTVLVSFYSSATGPKSVWYRIAFWLOWFNSFVNPLY 358
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Db 359 PLCHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 6
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match 66.9%; Score 1370.5; DB 12; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMLSSFAFAMVGNVILAFVVDRLHRSNYFFNLNLAIS 60
Db 1 MPTNSTINLSLSTKVTILAFFMSLVAFAMLGNALVILAFVVDKRLHRSYFFNLNLAIS 60
QY 61 DFLVGLISIPLYIDHVLNNNFGSGICMFWLITDYLCTASVYINVLISIDRYOSVNAV 120
Db 61 DFFVGVISIPLYIPIHTLFEWDFGKEICVFWMITDYLCTASVYINVLISIDRYLSVNAV 120
QY 121 SYRAQHTGIMKIVAMVAVILAFVNGPMLASDWNKSNNTKDCBPGFVTEWILIT 180
Db 121 SYRQHTGVILKIVLMAVAVLAFVNGPMLVSESWKDEGS--ECRPGFFSEWYILAIT 178
QY 181 MLLEFLLPVISVAFNVQIYWSLWKRRALSRCPHAGFSTTSSSAGSHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAFYNNIYWSLWKRDHLRCQHPGLTAVSSNICGHSFRGLSRSL 238
QY 241 PCLKESAAARHSESPPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESALRQREYAEELRG 300
Db 239 SASTVEVPASFHSEORRRKSSLMFSSRTKNSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLOWFNSFVNPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTVLVSFYSSATGPKSVWYRIAFWLOWFNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db 359 PLCHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 7
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PCI0963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

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Query Match      66.9%; Score 1370.5; DB 13; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMGVNAVILAFVVDNRLHRSSYFFFLNLAIS 60
DB 1 MPDNTSTINLSLSTRVTLLAFMGLVAFAMLGNAVLILAFVVDNRLHRSSYFFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVLISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLTASDKNSNTKDCBGFVTEWVILIT 180
DB 121 SYRTOHTGVLKIVLMVAVVILAFVNGPMLTASDKNSNTKDCBGFVTEWVILIT 178
QY 181 MLLEFLLPVISVAYFNVOIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVPIVLVAYFNWNIYWSLWKRRDLSCQHPGLTAVSSNICGHSFGRLLSSRRSL 238
QY 241 PGLKESAAHSRSPRRKSSILVSRTHMNSSITAFKVGSPWRSSEAAALROREYAEILLRG 300
DB 239 SASTEVPAFSPHSEQRQRKSSLMFSSRTKMSNTTASKMGFSQSDSVLHOREHVELLRA 298
QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPAALSO-NOSVSS 391
DB 359 PLCHKRFQKAFKLFICIKQPLPSQHSRSVSS 390

RESULT 8
US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US2003013798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match      66.9%; Score 1370.5; DB 14; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMGVNAVILAFVVDNRLHRSSYFFFLNLAIS 60
DB 1 MPDNTSTINLSLSTRVTLLAFMGLVAFAMLGNAVLILAFVVDNRLHRSSYFFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVLISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLTASDKNSNTKDCBGFVTEWVILIT 180
DB 121 SYRTOHTGVLKIVLMVAVVILAFVNGPMLTASDKNSNTKDCBGFVTEWVILIT 178
QY 181 MLLEFLLPVISVAYFNVOIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRTSN 240
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DB 179 SFLEFVPIVLVAYFNWNIYWSLWKRRDLSCQHPGLTAVSSNICGHSFGRLLSSRRSL 238
QY 241 PGLKESAAHSRSPRRKSSILVSRTHMNSSITAFKVGSPWRSSEAAALROREYAEILLRG 300
DB 239 SASTEVPAFSPHSEQRQRKSSLMFSSRTKMSNTTASKMGFSQSDSVLHOREHVELLRA 298
QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPAALSO-NOSVSS 391
DB 359 PLCHKRFQKAFKLFICIKQPLPSQHSRSVSS 390

RESULT 9
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-14

Query Match      66.9%; Score 1370.5; DB 14; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMGVNAVILAFVVDNRLHRSSYFFFLNLAIS 60
DB 1 MPDNTSTINLSLSTRVTLLAFMGLVAFAMLGNAVLILAFVVDNRLHRSSYFFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVLISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLTASDKNSNTKDCBGFVTEWVILIT 180
DB 121 SYRTOHTGVLKIVLMVAVVILAFVNGPMLTASDKNSNTKDCBGFVTEWVILIT 178
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[illegible]

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RESULT 10
US-10-354-769-2
; Sequence 2, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-769-2

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Query Match	66.9%;	Score 1370.5;	DB 14;	Length 390;
Best Local Similarity	68.1%;	Pred. No. 3.2e-119;		
Matches	267;	Conservative 40;	Mismatches 82;	Indels 3; Gaps 2
QY	1	MSESNTGTLPAQAQYPLAFMSSFAFAFMGNVAVILAFVVDRLNLRHRSYFFNLNLAIS	60	
DB	1	MPDNTNINLUSRVTLLAFFLSVLAFAFMGNALVILAFVVDKLNLRHRSYFFNLNLAIS	60	
QY	61	DFLVGISIPLXIYPHVLFWNNFGSGICFWLITDYLCTASVYINVLISYDRYQSVSNV	120	
DB	61	DFPVGVISIPLXIYPHTLFEWDGKCEVFLATDYLCTASVYINVLISYDRYLSVSNV	120	
QY	121	SYRAQHTGMKIVAQVAVWILAFYNGMILASDSWKSTNTKCEPGFVTEWYLTIT	180	
DB	121	SYRTQHTGVLKIYTLVAVWVLAFLYNGMILVSESQKDEGS--ECEPGFFSEWYLTAT	178	
QY	181	MILEFLLPVISVAFYFVNOIYWSLWKRRALSRCPSHAGFSTTSSASGHILHRAGVACRTSN	240	
DB	179	SFLFVIPVLVAFYFNWNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLRSRRSL	238	
QY	241	PGHKESAASHSPSRPKKSILVSLRPTHNNSSITAFKVGSWFSESAALRQREYAEILRG	300	
DB	239	SASTVEVPASPHERQRKRSKLSMFSSRTKMNSTNTASKMGFSQSDSVLAHQREHVELLRA	298	
QY	301	RKLARSAILLSAFACWAPYCVLFTIVLSTYPRTEPKSVVYISIAFWLOWFNSFVNPFY	360	
DB	299	RRLAKSAIILGVFAVCWAPYSLFTVILSFYSATGPKSVVYIRIAFWLOWFNSFVNPFY	358	

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QY      361 PLCHRFQFAFWKILCVTKWPALSQ-NQSVS 391
       |||||:|||||:|||||:|||||:|||||:
Db      359 PLCHKRFQFAFLKIFCIKKOPLFSQRSVSS 390

RESULT 11
US-10-393-807-14
; Sequence 14, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chong W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-14

Query Match          66.9%; Score 1370.5; DB 14; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY      1 MSESNSTGILPPAAOVPIAFIMSGSFAPAIWGNVAIVILAFVVDNRNLHRSNYFFLNLAIS 60
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MPDTNSTINLSLSTRVTLLAFMFSLVAFAMLGNALVILAFVVDKNLRHRSSYFFLNLAIS 60
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 DFLVGLSITPLYPHVLNNWFNGSGICFMFLTIDYLLCTASVYNIVLISDYRYSQSVNAV 120
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 DDFVGVISIPLYPHLTLEFWDGFKELCVFNLTDDYLLCTASVYNIVLISDYRLSVNAV 120
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      121 SYRAQHTGIMKIYAQMVAWVILAFVLNGPMILADSWKNXNTNKDCPCPGFTWEWILTIT 180
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 SYRTQHTGVKLVIITLMVAWVILAFVLNGPMILIVSESKDEGS--ECEPGFTSEWYLIAIT 178
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      181 MLLEFLLPVIYAVNFVQIYWLSLWKERALSRCPSHAGFTSTSSASGHLLRHAGVACRTSN 240
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      179 SFLEFVIPILYAVFNMMNIYWSLWKRDHLRSQCSPHPGLTAVSSNICGHSFGRLSSRSL 238
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      241 PGLKESAAGRSHGESPRKKSIIYSLRTHNMNSITAFKYGSPWRSSAALRQREVAELLRG 300
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      239 SASTEPDASFHERQRKRKSSLFESSFTKWNSTIASKGFSQSDVALHQEHVELLRA 298
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      301 RKLARSIALILLSAFACWAPCYCLFITVLSTYPTERTPKSVWYSIAFWLCWENSFVNPFY 360

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Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVMYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQAFWKILCFIKKQPLPSQHSRSVSS 390

RESULT 12
US-10-417-820A-14
; Sequence 14, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-14

Query Match 66.9%; Score 1370.5; DB 15; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNNAVILAFVVDNRNLRHSNFFFLNLAI 60
Db 1 MPDTNSTINLSLSTRVTLAFVSLVAFALMGNALVILAFVVDKNLRHRSYFFFLNLAI 60
QY 61 DPLVGLISIPLYPHVLFNWFNGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYPHLTFEWDGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVAQWAVVILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVLMVAVVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAI 178
QY 181 MLLEFLLPVISVAYNVQIYSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAYFMNIYSLWKRDHLSCQSPHGLTAVSSNICGHSFRGRUSSRSL 238
QY 241 PGLKESAAHSRSESPRRKSSILVSLRTHMNSSITAFKVGSWRSESAALRQRYAEALLRG 300
Db 239 SASTEVPASFHSEQRKRKSLMFSSRTKNSNTIASKMGFSQSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVMYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQAFWKILCFIKKQPLPSQHSRSVSS 390

RESULT 14
US-10-723-955-14
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Db 239 SASTEVPASFHSEQRKRKSLMFSSRTKNSNTIASKMGFSQSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVMYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQAFWKILCFIKKQPLPSQHSRSVSS 390

RESULT 13
US-10-696-673-2
; Sequence 2, Application US/10696673
; Publication No. US20040105846A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: PHRM0025-101/00231REGUS.1 DVI
; CURRENT APPLICATION NUMBER: US/10/696,673
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/203,108
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/852,165
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-696-673-2

Query Match 66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNNAVILAFVVDNRNLRHSNFFFLNLAI 60
Db 1 MPDTNSTINLSLSTRVTLAFVSLVAFALMGNALVILAFVVDKNLRHRSYFFFLNLAI 60
QY 61 DPLVGLISIPLYPHVLFNWFNGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYPHLTFEWDGKEICVFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVAQWAVVILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVLMVAVVILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAI 178
QY 181 MLLEFLLPVISVAYNVQIYSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAYFMNIYSLWKRDHLSCQSPHGLTAVSSNICGHSFRGRUSSRSL 238
QY 241 PGLKESAAHSRSESPRRKSSILVSLRTHMNSSITAFKVGSWRSESAALRQRYAEALLRG 300
Db 239 SASTEVPASFHSEQRKRKSLMFSSRTKNSNTIASKMGFSQSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVMYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQAFWKILCFIKKQPLPSQHSRSVSS 390

RESULT 14
US-10-723-955-14
```

Sequence 14, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruinsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled Receptors
FILE REFERENCE: 7.US29.CON
CURRENT APPLICATION NUMBER: US/10723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-955-14

Query Match 66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRLHRSNYFFNLALS 60
Db 1 MPTDNTINLSLSTRVTLAFMSSFAFAMVGNVILAFVVDNRLHRSNYFFNLALS 60
QY 61 DFLVGLISIPLYIPHLFNNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVYINVLISYDRYQSVNAV 120
QY 121 SYRAOHTGIMKIVAOVAVWILAFVNGFPMILASDSWKNSTNTKDCPGFVTEWYILTIT 180
Db 121 SYRTOHTGVKLIVLMVAVWVILAFVNGFPMILVSVESWKNDEGS--ECEPGFSEWYILAIT 178
QY 181 MLEFLLEPVISVAYFNVOIYWSLWKRRALSRCPSPHAGFTSTSSASGHLHRAVACRTSN 240
Db 179 SFLEFVIPVLVAYFNNNIYWSLWKRDHLSCQSPHGLTAVSSNTCGHSFGRLSRRSL 238
QY 241 PGLKESAAHSESPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAGFHSERQRRKSSLMFSSRTKXNSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 391
Db 359 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 390

Search completed: October 1, 2004, 10:22:50
Job time : 136 secs

Sequence 14, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruinsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled Receptors
FILE REFERENCE: 7.US29.CON
CURRENT APPLICATION NUMBER: US/10723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-955-14

Query Match 66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRLHRSNYFFNLALS 60
Db 1 MPTDNTINLSLSTRVTLAFMSSFAFAMVGNVILAFVVDNRLHRSNYFFNLALS 60
QY 61 DFLVGLISIPLYIPHLFNNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVYINVLISYDRYQSVNAV 120
QY 121 SYRAOHTGIMKIVAOVAVWILAFVNGFPMILASDSWKNSTNTKDCPGFVTEWYILTIT 180
Db 121 SYRTOHTGVKLIVLMVAVWVILAFVNGFPMILVSVESWKNDEGS--ECEPGFSEWYILAIT 178
QY 181 MLEFLLEPVISVAYFNVOIYWSLWKRRALSRCPSPHAGFTSTSSASGHLHRAVACRTSN 240
Db 179 SFLEFVIPVLVAYFNNNIYWSLWKRDHLSCQSPHGLTAVSSNTCGHSFGRLSRRSL 238
QY 241 PGLKESAAHSESPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAGFHSERQRRKSSLMFSSRTKXNSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 391
Db 359 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 390

Search completed: October 1, 2004, 10:22:50
Job time : 136 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:07:13 ; Search time 18 Seconds
(without alignments)
2089.494 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78.*

2: PIR1.*

3: PIR2.*

4: PIR3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1370.5	66.9	390	2 JC7566	histamine H4 recep
2	413	20.2	460	2 A24325	muscarinic acetyl
3	413	20.2	460	2 S09508	muscarinic acetyl
4	410.5	20.0	531	2 JT0531	muscarinic acetyl
5	410.5	20.0	590	2 S01114	muscarinic acetyl
6	410	20.0	460	2 A29514	muscarinic acetyl
7	410	20.0	460	2 IS1837	muscarinic recept
8	409.5	20.0	590	2 S47572	muscarinic acetyl
9	403	19.7	589	2 A29476	muscarinic acetyl
10	402.5	19.7	590	2 S10128	muscarinic acetyl
11	402	19.6	589	2 B29514	muscarinic acetyl
12	401	19.6	639	2 A55019	muscarinic acetyl
13	400	19.5	460	2 A31897	muscarinic acetyl
14	399.5	19.5	532	2 JT0530	muscarinic acetyl
15	392.5	19.2	477	2 S71323	muscarinic acetyl
16	392	19.1	490	2 A35546	alpha-1A adrenergi
17	390.5	19.1	400	2 G00013	muscarinic acetyl
18	390.5	19.1	501	2 JH0447	D3 dopamine recept
19	389.5	19.0	400	2 G01977	alpha-1A-adrenergi
20	389.5	19.0	515	2 A40491	d3 dopamine recept
21	388.5	19.0	491	2 A41632	alpha-1-adrenergi
22	388.5	19.0	572	2 I39369	histamine H1 recep
23	386.5	18.9	487	2 J2495	alpha-1A-adrenergi
24	385.5	18.8	488	2 I56507	histamine H1 recep
25	384.5	18.8	517	2 A45121	histamine H1 recep
26	382.5	18.7	560	2 A38731	alpha-1B adrenergi
27	382	18.7	479	2 S10127	alpha-1A adrenergi
28	380.5	18.6	466	2 S10126	muscarinic acetyl
29	380.5	18.6	501	2 T18863	hypothetical prote

ALIGNMENTS

RESULT 1

JC7566

histamine H4 receptor, HH4R - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C:Accession: JC7566

R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.

A:Biochem. Biophys. Res. Commun. 279, 615-620, 2000

A:Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.

A:Reference number: JC7566, MUID: 20568725; PMID:11118334

A:Contents: Leukocyte

A:Accession: JC7566

A:Molecule type: mRNA

A:Residues: 1-390 <NAK>

A:Cross-references: DDBJ:AB045370

C:Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled

C:Genetics:

A:Gene: hh4r

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 66.9%; Score 1370.5; DB 2; Length 390;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY	1	MSESNTGILPPAAQVPLAFMSFAIMGVNAVILAFVVDRLNRHRSNYFFELNLAI	60
DB	1	MPDTNSTINLSLSTRVTLAFMSLVAFALMGNALVILAFVVDKLRHRSYFFELNLAI	60
QY	61	DFVLGLISIPYIPHLVFNWFGSGICMFWLITDYLCTASVYNTVLISYDRYQSVNAV	120
DB	61	DFVGVISIPYIPHTLPEWDFGKEICVFWLTDDYLCTASVYNTVLISYDRYQSVNAV	120
QY	121	SYRAQHTGMKIVAOVAVILAFVNGPMILASDKNSNTKDCPCGFVTEWILIT	180
DB	121	SYRTQHTGVKLIVTLAVVAVLAFVNGPMILASDKNSNTKDCPCGFVTEWILIT	180
QY	181	MLLELLPVISVAYENVQIYMSLWKRRLSRCPHAGFTSTSSASGHLHRAGVACRTSN	240
DB	179	SFLEFVPIVILVAYVNNIYMSLWKRDLHRSQHPGUTAVSSNCGHSFRGLSRSL	238
QY	241	PLKESASRHSRSPRRKSSILVSLRTHMNSITAFKVGFSFWRSESAALRQREYALLRG	300
DB	239	SASTEVPASFSERQRRKSSLMFSRTQMNNTIASKMGSQSDSVLHQREHVELLRA	298
QY	301	RKLARSAILLSAFACWAPYCLFTIVLSTPRTPKSVWYSIAFWLQWNSFNWPLY	360
DB	299	RRLAKSAILLGAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFNWPLY	358
QY	361	PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391	
DB	359	PLCHKRQKAFKIFCIKKQLPLSQHSRSVSS 390	

[illegible]

RESULT 6
A29514
muscarinic acetylcholine receptor M1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C:Accession: A94518; A94293; A37121; A29514
R:Bonner, T.I.
submitted to GenBank, July 1987
A:Reference number: A94518
A:Accession: A94293
A:Molecule type: mRNA
A:Residues: 1-460 <B01>
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
A:Reference number: A94293; MUID:87263421; PMID:3037705
A:Accession: A94293
A:Molecule type: mRNA
A:Residues: 1-227;338-460 <B02>
A:Experimental source: cerebral cortex
A:Note: only a part of the protein translation is given; none of the nucleotide sequence
R:Kurténbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: A37121
A:Status: preliminary
A:Molecule type: protein
A:Residues: 62-124 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>
F:2.12/Binding site: carbohydrate (Asn) #status predicted

Query Match 20.0%; Score 410; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 1.7e-27;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;
Qy 5 NSTGILPPAAQVPLAFL---MSSFAFAMVGNNAVILAFVVDRLRHSNFFFLNLAISD 61
Db 12 NITVLAPGKGPQVAFIGITIGLLSLATVTGNLLVLSFKVNTLKTNNYFLLSLACAD 71
Qy 62 FLVGLISIPLYIPHLVFNWFGSGICMFMFLITDYLLCTASVYNIVLISYDRYQSVNAV 120
Db 72 LIIGTFSMNLYTTLGMHGWALGTACDLWALDYVNASVNMNLLISFDYFVSFVTRPL 131
Qy 121 SYRAQHTGIMKIVAOVAV-WILAFVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
Db 132 SYRAKET--PRAALMIGLAWLVSFVLWAPAIL---FWQYLVGERTVLAGQCYIQFLSOP 186
Qy 175 YILITMTLLEFLLPVISVAYFNVOIYWSLWKR-----RAL-----SRCPSHAGFTTSSS 224
Db 187 IITFGTAMAAFYLPVTVMC-----TLYWRITYETENRARELAALQSGETPGKGGSSSSSE 242
Qy 225 AS-----GHLHRAGVACRT-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294
Db 243 RSQPGAEGSPSPGRCR---CCRAPRLLOAYSWKEEEDEGSMESLTSSEGEPEP--G 297
Qy 259 SSILVSL-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294
Db 298 SEVVIKMPVDSQAQPTKQPPKSSPNTVKRPTKKG---RDRGGKGQKPRGKEQLAKRKT 354
Qy 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSF 354
Db 355 FSLVKEKAARTLSAILLAFILTWTPYINWLV-STFCKDCVPETLW-ELGYWLCVNST 412
Qy 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
Db 413 VNPFCYALCNKAFRTDF-RLILLCRW 437

RESULT 8
S47572
muscarinic acetylcholine receptor m3 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 18-Feb-2000
C:Accession: S47572
R:Blee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
Biochim. Biophys. Acta 1223, 151-154, 1994
A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re
A:Reference number: S47572; MUID:94339178; PMID:8061048
A:Accession: S47572
A:Status: preliminary
A:Molecule type: mRNA

Db 413 VNPFCYALCNKAFRTDF-RLILLCRW 437

RESULT 7
I51837
muscarinic receptor - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text_change 24-Nov-1999
C:Accession: I51837
R:Lai, J.; Smith, T.B.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske,
Adv. Exp. Med. Biol. 287, 313-330, 1991
A:Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy
A:Reference number: I51837; MUID:92101806; PMID:1759615
A:Accession: I51837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <RES>
A:Cross-references: GB:S73971; NID:G241253; PIDN:AAB20705.1; PID:G241254
C:Genetics:
A:Gene: m1
C:Superfamily: vertebrate rhodopsin

Query Match 20.0%; Score 410; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 1.7e-27;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;
Qy 5 NSTGILPPAAQVPLAFL---MSSFAFAMVGNNAVILAFVVDRLRHSNFFFLNLAISD 61
Db 12 NITVLAPGKGPQVAFIGITIGLLSLATVTGNLLVLSFKVNTLKTNNYFLLSLACAD 71
Qy 62 FLVGLISIPLYIPHLVFNWFGSGICMFMFLITDYLLCTASVYNIVLISYDRYQSVNAV 120
Db 72 LIIGTFSMNLYTTLGMHGWALGTACDLWALDYVNASVNMNLLISFDYFVSFVTRPL 131
Qy 121 SYRAQHTGIMKIVAOVAV-WILAFVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
Db 132 SYRAKET--PRAALMIGLAWLVSFVLWAPAIL---FWQYLVGERTVLAGQCYIQFLSOP 186
Qy 175 YILITMTLLEFLLPVISVAYFNVOIYWSLWKR-----RAL-----SRCPSHAGFTTSSS 224
Db 187 IITFGTAMAAFYLPVTVMC-----TLYWRITYETENRARELAALQSGETPGKGGSSSSSE 242
Qy 225 AS-----GHLHRAGVACRT-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294
Db 243 RSQPGAEGSPSPGRCR---CCRAPRLLOAYSWKEEEDEGSMESLTSSEGEPEP--G 297
Qy 259 SSILVSL-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294
Db 298 SEVVIKMPVDSQAQPTKQPPKSSPNTVKRPTKKG---RDRGGKGQKPRGKEQLAKRKT 354
Qy 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSF 354
Db 355 FSLVKEKAARTLSAILLAFILTWTPYINWLV-STFCKDCVPETLW-ELGYWLCVNST 412
Qy 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
Db 413 VNPFCYALCNKAFRTDF-RLILLCRW 437

A;Residues: 1-590 <JEE>
A;Cross-references: EMBL:U08286; NID:g520465; PIDN:AAA51866.1; PID:g520466
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match	20.0%	Score 409.5	DB 2	Length 590
Best Local Similarity	25.0%	Pred. No. 2.6e-27		
Matches 126	Conservative 83	Mismatches 134	Indels 151	Gaps 17
QY	18	LAFIMSSFAIMVGNVAVILAFVVDNRNLRHSYFFLNLAISDPLVLGISIPIYIPIHVL	77	
Db	71	I AELTGVLAIVTIIGNTLIVIAFVKVQKLTNNYFLLSLACAOLIIIGVISMNLFTVII	130	
QY	78	FN-WNFGSGICMEWLIIDYLLCTASVNVILVSDRYOSVNAVSYRAOHT----	132	
Db	131	MNRWALGNLACDLWLSIDYVASVNVNLLVSDRFYSITRPTUYAKRTTKDAGVNI	190	
QY	133	VAQWVAVIILAFIVGPMILASDWKNTSTKDCPEG-----FVTEWVILITITMLEFL	187	
Db	191	LA-----WVLSFILWAPAIL---FWQYFVKRTVPPGCEFIQLSEFIITFGTAIAFY	242	
QY	188	PVISAFAVNVQIYKSLWKRALRCRSHAGF---STTSSASGHLHRAGVACRTSNPGL	245	
Db	243	PVTIMTI-----LYWRIYKETE-KRTKELAGLQASGEAAEENFVHPGTSSRSSYELQ	297	
QY	246	SAASR-----HSES-----	254	
Db	298	QSMKRSARRKYGRCHFETTKSWKPAEQDQDQHSDDSNWNNDAASLENSASSDEE	357	
QY	255	----PRKKSILVSLRTH---MNS-----SITAPKY-----	278	
Db	358	GSETRAIYIVLKLPGHSTILNKLPSDDLQVPEELSGVLERKPSKLQTSQSMDDG	417	
QY	279	GSFWRS-----ESAA-----	291	
Db	418	GSFQKSFSLQLESADVDTAKASDVNSVVGKTTATPLSFKEATLAKRFALKTRSQIT	477	
QY	292	REYAEILRRGKLARSIAILLASFAICWAPYCLFTIIVLSTPRTERPKSVWYSIAFWLQ	351	
Db	478	KRKMSLIKEKKAQTLISALLAFIITWTYINMVLV-NTFCDSICPKTYW-NLGYWLCY	535	
QY	352	NSFVNPFLYPLCHRRFPQKAFWIL	375	
Db	536	NSTVNPVCYALCNKTFPRNTFMML	559	

RESULT 9
A29476
muscarinic acetylcholine receptor M4 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
#Accession: A29476
A:Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A:Title: A novel subtype of muscarinic receptor identified by homology screening.
A:Reference number: A29476; MUID:88077069; PMID:3120722

Accession: A29476
Molecule type: mRNA
Residues: 1-589 <BRA>
Cross-references: GB:M18088; NID:g202657; PIDN:AAA0659.1; PID:g202658
Experimental source: brain
Superfamily: vertebrate rhodopsin
Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane #status predicted <TM1>
Domain: transmembrane #status predicted <TM2>
Domain: transmembrane #status predicted <TM3>
Domain: transmembrane #status predicted <TM4>
Domain: transmembrane #status predicted <TM5>
Domain: transmembrane #status predicted <TM6>
Domain: transmembrane #status predicted <TM7>

Query Match 19.7%; Score 403; DB 2; Length 589;
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Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;

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QY 4 SNGTGILPPAAQ-----VELAFLMSSFAFAFMGVNAVILAFVVDENLPHRSNYFFLNLA 58
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
51 SNTSDPGLGHTIWQVFFIAFLTGFLVLTIIIGNILVIAFKVKQKLTAVNYFLLSLA 110
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
59 ISDFVLGLISIPYIYHFLFN--MNFSGIGCMFWLITDYLLCTASVYNTLISYDRYQSVS 117
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
111 CADLIIGVISMNLFTTVIIMRWALGNLACDLWLSIDYVNASVWMLIVISDFRYSIT 170
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
118 NAVSYEAOHT-----GIMKIVAOVAVVILAFVNGPMILASDSWKNSNTTKDCBPG--- 169
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
171 RPTVYRAKRTTKRAGVWIGLA-----WVISFLWAPAIL---FWQYFVGKRTVPGECFI 222
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
170 -FVTEWVYILITMLLEFLLPVISVAYENVOLYWSLWKRRALSRCPSHAGF--STTSSAS 226
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
223 QFLSEPTITFGYIAAFYEVMTIMTI-----LYMKRIYKETE-KRTKELAGLOASGTAEAAE 277
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
227 GHLHRAGVACRTSNPGLKESAAASHESPRRK-----SSRKYGRCHFWFTTKSWKPABEQMDQDHSSSD 258
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
278 NFVHPGTSSRSCSYELQQQGVKR---SSRKYGRCHFWFTTKSWKPABEQMDQDHSSSD 334
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
259 -----SSILVSLRTHMNSSI----- 273
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
335 SWNNDDAAASLENSASSDEBDIGSETRAYISIVKLPGHSSILNSTKLPSDNLQVSNED 394
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
274 -----TAPKVGGSFWSESAA----- 288
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
395 LGTVDVVERNAHKLQAKSGMDGDNCKODFTKLPIQLSEAVDTGKTSNTSSADKTTATLP 454
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
289 -----LRQREYABLGRKLARSAILLSAFAICWAPYCLTIVLS 329
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
455 LSFKEATLAKRFALKTRSQITKRRKSLIKEKAAQITLSALLAFIITWYINWLVV-N 513
QY      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
330 TYPRTERPKSVWYSTAFWLQWNSFVNPFLYPLCHRRFQKAFKIL 375
Db      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
514 TFRDSCIPKTYW-NIGYWLICYINSTVNPVCYALCNKTRFTTFKMLL 558

RESULT 10
S10128
muscarinic acetylcholine receptor M4 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Feb-2000
C:Accession: S10128
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of human muscarinic acetylcholine receptor subtypes.
B:Reference number: S04326; MUID:8616632; PMID:3443095
```

RESULT 10

S10128
muscarinic acetylcholine receptor M4 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Feb-2000
C:Accession: S10128
R:Peralka, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of the human muscarinic acetylcholine receptor subtypes M1-M4
A:Reference number: S04326; MUID:88166632; PMID:3443095
A:Accession: S10128
A:Molecule type: DNA
A:Residues: 1-590 <PER>
A:Cross-references: EMBL:X15266; NID:G32323; PIDN:CAA33337.1; PID:G32324
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein
F:68-95/Domain: transmembrane #status predicted <TM1>
F:105-131/Domain: transmembrane #status predicted <TM2>
F:143-164/Domain: transmembrane #status predicted <TM3>
F:185-207/Domain: transmembrane #status predicted <TM4>
F:231-252/Domain: transmembrane #status predicted <TM5>
F:493-513/Domain: transmembrane #status predicted <TM6>
F:525-546/Domain: transmembrane #status predicted <TM7>
F:5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match      19.7%; Score 402.5; DB 2; Length 590;
Best Local Similarity 24.08; Pred. No. 1e-26;
Matches 121; Conservative 86; Mismatches 135; Indels 163; Gaps 16;

QY      18  LAFIMGSFAFAMVGNAAVIAFAVVDRLNRHSYFFNLALAISDFLVLGSLXPVHVL 77
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Db      71  IAEFTGILATVTIIGNILVIVSFKNQKLVKNVNFLLSLACADLIIGVISMNLFYYII 130

QY      78  FN-WNFGSGICMFWLITDYLCLLTASVNIVLISYDRYQSVSNVSYRAQHT----GIMKI 132

```


Db 131 MNRWALGNLACDLWLAIDYVYASVWMLLVISFDRIYFSITRLTTRAKTKRAGWMIG 190
 QY 133 VAQWVAVWILAFVNGPMILASDWSKNTKDCPEG-----FVTEWYILITMLLEFLL 187
 Db 191 LA-----WVLSFVWAPAIL---FWQYFVGKRTVPGECEFIQFLSEPTITFGTAIAAFYM 242
 QY 188 FVTSVAVFNVOIYWSLWK----- 205
 Db 243 PVTIMTI---LYWRIYKETEKRTELKELAGLQASGTEAETENFVHPTGSSRSCSSYELQOQ 298
 QY 206 -----RRALSRCPHAGPFTT-----SSASCHLRHAGVACKTSNPGKLES 246
 Db 299 SMKRSNRKRGRC--HFVFTKSWKPSSEQMDQDHSSDSDWNNDDAAASLENSASSDEED 356
 QY 247 AASR-----HS----- 252
 Db 357 IGSETRAIYSIVLKLPGHSTILNSTKLPSDDNLQVPEELGMVDLKERKADKLQAKSVDD 416
 QY 253 --ESPRLKSSILVSLR-----THNNSI-----TAFKVGSS-----FWRSESAALR 290
 Db 417 GGSFPKFSKPLIQLESADVDTAKTSDVNSVSGKSTATLPLSFKEATLAKRFALKTRSQIT 476
 QY 291 QREYAEILLRGRKLARSAILLSAFACWAPYCLFTIVLSTVPTPRTERPKSVWYSIAFWLQW 350
 Db 477 KRKMSLVKEKAAQATLSAAILAFITITWPNIMVLV-NTFCDSCIPKTFW-NLGYWLCY 534
 QY 351 FNSFVNPLYPCHRRFOKAFWKIL 375
 Db 535 INSTVNPVCYALCNKTFRTFMQLL 559
 RESULT 11
 B29514
 Muscarinic acetylcholine receptor M3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000
 C:Accession: B94518; B94293; B37121; B29514
 R:Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: B94518
 A:Molecule type: mRNA
 A:Residues: 1-589 <BO1>
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:87263421; PMID:3037705
 A:Accession: B94293
 A:Molecule type: mRNA
 A:Residues: 1-269;463-589 <BO2>
 A:Experimental source: cerebral cortex
 A:Note: only a part of the protein translation is given; none of the nucleotide sequence
 R:Kartenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: B37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 104-166 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
 F:67-90/Domain: transmembrane #status predicted <TM1>
 F:104-124/Domain: transmembrane #status predicted <TM2>
 F:142-163/Domain: transmembrane #status predicted <TM3>
 F:184-206/Domain: transmembrane #status predicted <TM4>
 F:230-251/Domain: transmembrane #status predicted <TM5>
 F:492-512/Domain: transmembrane #status predicted <TM6>
 F:527-545/Domain: transmembrane #status predicted <TM7>
 F:6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 19.6%; Score 402; DB 2; Length 589;

Best Local Similarity 23.8%; Pred. No. 1.1e-26;
 Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;
 QY 4 SNSTGLPPAAQ-----VPLAFLMSSFAFPAIMVGNVAVILAFVVDRLNLRHSNYFFLNLA 58
 Db 51 SNTSDPLGGHTIMQVVFIAFTGLAVTIIGNILVIVAFKVNKQKLTNNVFLSLA 110
 QY 59 ISDFLVGLISIPLYIPHLFN-WNFGSGICMFWLITDYLLCTASVNVILISVDRIQSVS 117
 Db 111 CADLIIGVISMNLFTTIIIMRWALGNLACDLWLSIDYASVWMLLVISPDYFSIT 170
 QY 118 NAVSYRAQHT-----GINKIYAVQWVAVILAFVNGPMILASDWSKNTKDCPEG--- 169
 Db 171 RPLTYRAKRTTKRGGVMIGLA-----WVLSFVWAPAIL---FWQYFVGKRTVPGECEFI 222
 QY 170 -FVTEWYILITMLLEFLLPVISVAVFNVOIYWSLWKRRALSRCPHAGF--STTSSAS 226
 Db 223 QFUSEPTITGTAIAAFYMPVTIMTI---LYWRIYKETE-KRTKELAGLQASGTEAEAE 277
 QY 227 CHLRAGVACRTSNPGKESAAASHSESPPRK----- 258
 Db 278 NFVHTGSSRSCSSYELQOQGVKR---SSRRKYGRCHFVFTTKSWKPSAEQMDQDHSSD 334
 QY 259 -----SSILVSLRTHMNSI----- 273
 Db 335 SWNNDDAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSSILNSTKLPSDDNLQVSNED 394
 QY 274 -----TAFKVGFSFWRSESA----- 288
 Db 395 LGTVDVVERNAHKLQAKSMGDCNQCKQFTKLPLOLESADVDTGKTSNTSSADKTTATLP 454
 QY 289 -----LRQRYAEALLRGRKLARSAILLSAFACWAPYCLFTIVLS 329
 Db 455 LSFKEATLAKRFALKTRSQITKRRKMSLIKEKAAQATLSAAILAFITITWPNIMVLV-N 513
 QY 330 TYPRTERPKSVWYSIAFWLQWNSFVNPLYPCHRRFOKAFWKIL 375
 Db 514 TFCDSICPIKTFW-NLGYWLCYINSTVNPVCYALCNKTFRTFTFKILL 558
 RESULT 12
 A55019
 Muscarinic acetylcholine receptor, M3 isoform - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A55019
 R:Gadbut, A.P.; Galper, J.B.
 J. Biol. Chem. 269, 25823-25829, 1994
 A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and
 A:Reference number: A55019; MUID:95014393; PMID:7929287
 A:Accession: A55019
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-639 <GAD>
 A:Cross-references: GB:110617; NID:9530097; PIDN:AAA65961.1; PID:9530098
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor
 Query Match 19.6%; Score 401; DB 2; Length 639;
 Best Local Similarity 24.4%; Pred. No. 1.5e-26;
 Matches 124; Conservative 84; Mismatches 136; Indels 164; Gaps 16;
 QY 16 VPLAFLMSSFAFPAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAISDFLVGLISIPLYI 75
 Db 117 VLIATLGIATLVIIGNILVIVSFKNQKLTNNVFLSLACADLIIGVISMNLFTTY 176
 QY 76 VLF-WNFGSGICMFWLITDYLLCTASVNVILISVDRIQSVSNVYRAQHT-----GIM 130
 Db 177 IIMGHWALGNLACDLWLSIDYASVWMLLVISPDYFSITRPTTYRAKRTTKRAGVM 236
 QY 131 KIYAVQWVAVILAFVNGPMILASDWS-----KNSTNTKDCPEGFVTEWYILITMLLEF 185
 Db 237 IGLA-----WVLSFVWAPAIL---FWQYFVGKRTVPDLDECFTQFLSEPTITFGTAIAAF 288

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QY 186 LLPVISAAYFNQVYIWSLWKRALSRCPSHAGFSTSSA--SGHLHRAGVACRTSNGL 243
Db 289 YLPVTIMSI-----LYWRIYKETE-KRTKELAGLQASGEAETARVHVHTGSRSLSSYEL 343
QY 244 KESASRHSSESPRKS----- 259
Db 344 QRQSTKSSRRKRYRRCHFWLMTKSWEPNTDQDQEHSSSDWNNDAAASLSSASSDEE 403
QY 260 -----SILVSLRTH-----MNSSITAFKV----- 278
Db 404 DITAEITAIYSIVLKLPHSAILNSTKLPPSSDELNEGADLOKSDTSQEKKPKLOPPK 463
QY 279 -----GSFWS-----BSAAL----- 289
Db 464 SIQDGSFQKFSKLPQPGSAETATASDGISSVTKTSAAALPLSFKEATLAKKALKTRS 523
QY 290 --RQREYAEILRGKRLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFW 347
Db 524 QITRKRMSLIKKKAQCTISAILFAIITWTPTYNIMLV-NTFCDGV-PKTVN-NLGYW 580
QY 348 LOWFNSFVNPLPLCHRRRQKAFWKIL 375
Db 581 LCVINSTVNFVCAIOWKMFNTFQMLL 608

RESULT 13
A31897
muscarinic acetylcholine receptor M1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 24-Nov-1999
C:Accession: A31897
R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 263, 18397-18403, 1988
A:Title: Isolation, sequence, and functional expression of the mouse M1 muscarinic acetylcholine receptor.
A:Reference number: A92694; MUID:89054021; PMID:2848036
A:Accession: A31897
A:Molecule type: DNA
A:Residues: 1-460 <SHA>
A>Note: the authors translated the codon ATC for residue 119 as Thr
R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 264, 6596, 1989
A:Reference number: A92742
A:Contents: annotation; erratum, correct translation of residue 119
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphodiesterase; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphodiesterase
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>

Query Match 19.5%; Score 400; DB 2; Length 460;
Best Local Similarity 27.0%; Pred. No. 1.3e-26;
Matches 120; Conservative 86; Mismatches 152; Indels 86; Gaps 19;
QY 5 NSTGILPAAQVPLAFLMSS---FAFAMVGNVAVILAFVVDNLRHRSNYFFFLNLAISD 61
Db 12 NITVLAPKGPQVAFISTGTLGLSLATVTTGNLLISIKVNTLKTNNVFLSLACAD 71
QY 62 FLVGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNTVLISYDRYQSVSNV 120
Db 72 LIIGTFSMNLYTYLLMGHWALGTACDLNLDVYASVWNLIVISDFRYSITREITRAKTRPKRAGIM 150
QY 121 SYRAQHTGIMKIVQMVAW-VILAFVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
Db 132 SYRAKRT--PRAALMIGLAMVSPVLWAPALIL---FWQLVGERTVLVAGQCIQFLSQP 186
QY 175 YLITITMLELFLPVISVAYFNQVYIWSLWK-----RAL-----SRCPSHAGFSTSSS 224
Db 187 IITGTMAAFYLPVTVMC-----TLYWRIYRTENRARELAALQSGSETPGKGGGSSSSE 242

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QY 225 AS-----GHLHRAGVACRT-----SNPGLKESASRHSSESPPRK 258
Db 243 RSOPGAEGSPSPGPCRCR---CCRAPLLQAYSWKEEEDSGMESLTSSEGEP--G 297
QY 259 SSILVSL-----RTHMNSSITAFK-----VGSFWRSESALRQREYAE 296
Db 298 SEVVIKPMVDPEAQAPTKQPKSPNTVRPTTKGRDGGKQKPRGKEQMAKRKTFE- 356
QY 297 LLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSVN 356
Db 357 LVKEKKAARTLSAILLAFILWTPTYNIMLV-STFCKDCVPETLW-ELGYMLCYVNSTVN 414
QY 357 PFLYPLCHRRRQKAFWKILCVTKW 380
Db 415 FMCYASCNKAFRDHF-RLLLICRW 437

RESULT 14
JT0530
muscarinic acetylcholine receptor M5 - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C:Accession: JT0530
R:Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Neuron 1, 403-410, 1988
A:Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor.
A:Reference number: JT0530; MUID:90166521; PMID:3272174
A:Accession: JT0530
A:Molecule type: DNA
A:Residues: 1-532 <BON>
C:Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotransmitter acetylcholine.
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphodiesterase; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphodiesterase
F:30-53/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:105-126/Domain: transmembrane #status predicted <TM3>
F:147-169/Domain: transmembrane #status predicted <TM4>
F:192-214/Domain: transmembrane #status predicted <TM5>
F:444-464/Domain: transmembrane #status predicted <TM6>
F:479-498/Domain: transmembrane #status predicted <TM7>
F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.5%; Score 399.5; DB 2; Length 532;
Best Local Similarity 24.6%; Pred. No. 1.6e-26;
Matches 122; Conservative 90; Mismatches 142; Indels 141; Gaps 15;
QY 16 VPLAFIMSSFAFAMVGNVAVILAFVVDNLRHRSNYFFFLNLAISDPLVGLISIPLYIPH 75
Db 31 ITIAAVTAVVLIITVGNVLMISFKVNSQLKTVNNYLLSLACADLISGIFSMNLYTY 90
QY 76 VLF-NWNFGSGICMFWLITDYLLCTASVYNTVLISYDRYQSVSNVSYRAQHT---GTM 130
Db 91 ILMGRWALGSLACDLNLDVYASVWNLIVISDFRYSITREITRAKTRPKRAGIM 150
QY 131 KIVAQMVAWILAFVNGPMILASDSW-----KNSTNTKDCPEGFVTEWYILITMLLEF 185
Db 151 IGLA-----WLISFILWAPAILC---WQYLVGKRTVPLDECOIQISEPTITFGTAAAP 202
QY 186 LLPVISAAYFNQVYIWSLWK-----RALSRCP----- 213
Db 203 YIPVSMVITLCYRIRETEKTKDLADLQSDSVTKAEKRKPAHRAALFRSLCRLCPRTLA 262
QY 214 ---SHAGFSTT---SSASGHLHRAG-----VACRT-----SNPGLK 244
Db 263 QRERNQASWSSSRSTSTTGKPSQATGPSANWAKAEQUTTCSSYPSSDEDEKPADPVLQ 322
QY 245 ESASRHSSESPPRKSSILVSLRTHMNSSI--TAFKVGSGFWRSESAAALR----- 290
Db 323 VVYKSGKESGPEGSFSAETEETEVKAETEKSDYDTNLYLLSPAAHPRKSKQCVAYKFR 382
QY 291 -----OREYAEILRGRKLAR 305

```

Search completed: October 1, 2004, 10:13:03
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:05:12 ; Search time 13 Seconds
(without alignments)
1566.110 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAISQNSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1370.5	66.9	390	1	HH4R_HUMAN
2	722.5	35.3	445	1	HH3R_HUMAN
3	721.1	35.2	445	1	HH3R_CAVPO
4	716.5	35.0	445	1	HH3R_RAT
5	715.5	34.9	445	1	HH3R_MOUSE
6	418.0	20.4	460	1	ACM1_WACMU
7	414.5	20.2	532	1	ACM5_WACMU
8	413.0	20.2	460	1	ACM1_HUMAN
9	413.0	20.2	460	1	ACM1_PIG
10	410.5	20.0	531	1	ACM5_RAT
11	410.5	20.0	590	1	ACM3_PIG
12	410.0	20.0	460	1	ACM1_RAT
13	409.5	20.0	590	1	ACM3_BOVIN
14	408.0	19.9	585	1	ACM3_CAEEL
15	404.5	19.8	532	1	ACM5_HUMAN
16	404.0	19.7	589	1	ACM3_MOUSE
17	403.5	19.7	590	1	ACM3_PONPY
18	402.5	19.7	590	1	ACM3_GORGO
19	402.5	19.7	590	1	ACM3_HUMAN
20	402.5	19.7	590	1	ACM3_PANTR
21	402.0	19.6	589	1	ACM3_RAT
22	401.0	19.6	460	1	ACM1_MOUSE
23	401.0	19.6	639	1	ACM3_CHICK
24	394.5	19.3	576	1	AIAD_RABIT
25	393.0	19.2	444	1	OAR_CAEEL
26	393.0	19.2	562	1	AIAD_MOUSE
27	392.5	19.2	470	1	AIAD_ORYLA
28	392.0	19.1	490	1	ACM4_CHICK
29	390.5	19.1	400	1	D3DR_CERAE
30	389.5	19.0	400	1	D3DR_HUMAN
31	389.5	19.0	515	1	AIAB_MESAU
32	389.5	19.0	515	1	AIAB_RAT
33	388.5	19.0	491	1	HH1R_BOVIN

34	388.5	19.0	572	1	AIAD_HUMAN	P25100 homo sapien
35	388.0	18.9	488	1	HH1R_MOUSE	P70174 mus musculus
36	386.5	18.9	487	1	HH1R_HUMAN	P35367 homo sapien
37	386.5	18.9	487	1	HH1R_PANTR	Q9n2b2 pan troglod
38	385.5	18.8	488	1	HH1R_CAVPO	P31389 cavia porce
39	385.0	18.8	514	1	AIAB_MOUSE	P37717 mus musculus
40	384.5	18.8	519	1	AIAB_HUMAN	P35368 homo sapien
41	382.5	18.7	561	1	AIAD_RAT	P23944 rattus norv
42	382.0	18.7	479	1	ACM4_HUMAN	P08173 homo sapien
43	380.5	18.6	466	1	ACM2_HUMAN	P08172 homo sapien
44	380.0	18.6	432	1	A2AR_LABOS	Q91081 labrus ossi
45	379.5	18.5	466	1	ACM2_RAT	P10980 rattus norv

RESULT 1

HH4R_HUMAN STANDARD; PRT; 390 AA.

AC Q9H3N8; Q9GZQ0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)

DE (GPCR105) (SP9144) (AXOR35).

GN HRH4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

[1]_TaxID:9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=20538417; PubMed=10973974;

RA Oda T., Morikawa N., Saito Y., Matsumoto S.-I.;

RT "Molecular cloning and characterization of novel type of histamine receptor preferentially expressed in leukocytes.";

RL J. Biol. Chem. 275:36781-36786(2000).

[2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Leukocyte;

RX MEDLINE=20568725; PubMed=11118334;

RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;

RT "Molecular cloning and characterization of a new human histamine receptor, HH4R.";

RL Biochem. Biophys. Res. Commun. 279:615-620(2000).

[3]

RP SEQUENCE FROM N.A.

RA Jones P.G., Wu S., Betty M.;

RT "Cloning of a novel histamine receptor.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

[4]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Bone marrow;

RX PubMed=11179434;

RA Liu C., Ma X.-J., Jiang X., Wilson S.-J., Hofstra C.L., Blevitt J., Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;

RT "Cloning and pharmacological characterization of a fourth histamine receptor (H4) expressed in bone marrow.";

RL Mol. Pharmacol. 59:420-426(2001).

[5]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Eosinophil;

RX MEDLINE=21104636; PubMed=11181941;

RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A., Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N., Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M., Monsma F.O. Jr.;

RT "Cloning and characterization of a novel human histamine receptor.";

RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).

[6]

RP SEQUENCE FROM N.A.

RX MEDLINE=21106320; PubMed=11179436;

RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,
RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,
RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
RA Bergma D.J., Fitzgerald L.R.;
RT "Cloning, expression, and pharmacological characterization of a novel
RT human histamine receptor";
RL Mol. Pharmacol. 59:434-441(2001).
[7]
RN SEQUENCE FROM N.A.
RP O'Reilly M.A.;
RA "Identification of a histamine H4 receptor on human eosinophils - Role
RT in eosinophil chemotaxis";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[8]
RN SEQUENCE FROM N.A.
RP Publ H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The H4 subclass of histamine receptors could mediate the
CC histamine signals in peripheral tissues. Displays a significant
CC level of constitutive activity (spontaneous activity in the
CC absence of agonist).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and
CC eosinophils. Shows preferential distribution in cells of
CC immunological relevance such as T-cells, dendritic cells,
CC monocytes, mast cells, neutrophils. Also expressed in a wide
CC variety of peripheral tissues, including the heart, kidney, liver,
CC lung, pancreas, skeletal muscle, prostate, small intestine,
CC spleen, fetal liver and lymph node.
CC -!- INDUCTION: Expression is either up-regulated or down-regulated
CC upon activation of the lymphoid tissues and this regulation may
CC depend on the presence of IL-10 or IL-13.
CC -!- MISCELLANEOUS: Does not bind diphenhydramine, lorazepam,
CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity
CC for dimaprit, imipramine and imetit. The order of inhibitory activity
CC is imetit > clobenpropit > burinamide > thioetheramide.
CC Clobenpropit behaves as a partial agonist, dimaprit and
CC imipramine show some agonist activity while clozapine behaves as
CC a full agonist. Thioetheramide shows inverse agonism (enhances cAMP
CC activity). The order of inhibitory activity of histamine
CC derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-
CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-
CC methylhistamine > R(-)-alpha-methylhistamine behave as full
CC agonists.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

CC EMBL; AB044934; BAB13698.1; -;
CC EMBL; AB045370; BAB20091.1; -;
CC EMBL; AF307973; AAG32052.1; -;
CC EMBL; AF312230; AAK12081.1; -;
CC EMBL; AF328449; AAK43542.1; -;
CC EMBL; AF325356; AAL01684.1; -;
CC EMBL; AJ298292; CAC83493.1; -;
CC EMBL; AY136745; AAN01271.1; -;
CC PIR; JC7566; JC7566.
CC Genew; HGNC:17383; HRH4.
CC MIM; 606792; -; C: integral to membrane; NAS.
CC GO; GO:0016021; -; C: integral to membrane; NAS.
CC GO; GO:0004969; F: histamine receptor activity; NAS.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC InterPro; IPR008102; Histamine_H4.
CC Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PRINTS; PR01726; HISTAMINEH4.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 20 40 1 (POTENTIAL).
FT DOMAIN 41 52 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 53 73 2 (POTENTIAL).
FT TRANSMEM 74 87 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 88 108 3 (POTENTIAL).
FT TRANSMEM 109 131 4 (POTENTIAL).
FT TRANSMEM 132 152 5 (POTENTIAL).
FT TRANSMEM 153 172 6 (POTENTIAL).
FT TRANSMEM 173 193 7 (POTENTIAL).
FT TRANSMEM 194 304 8 (POTENTIAL).
FT TRANSMEM 305 325 9 (POTENTIAL).
FT TRANSMEM 326 341 10 (POTENTIAL).
FT TRANSMEM 342 362 11 (POTENTIAL).
FT TRANSMEM 363 390 12 (POTENTIAL).
FT DISULFID 87 164 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 374 374 S-palmitoyl cysteine (POTENTIAL).
FT CONFLICT 138 138 A -> V (IN REF. 1).
FT CONFLICT 206 206 H -> R (IN REF. 1).
FT CONFLICT 253 253 Q -> R (IN REF. 1).
SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;
Query Match 66.9%; Score 1370.5; DB 1; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-85;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSENSTGILPPAAQVPLAFMLSSFAFMVGNVAVILAFVVDRLNHRNVFFLNLAIS 60
DB 1 MPDNTSTINLSLSTRTVLAFFMFLVFAIMUGNALVILAFVVDKLNHRSSVFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHYLVFNFMNFGSGICMFWLITDYLLCTASVYINVLISYDRYSQVSNV 120
DB 61 DFFGVGISIPLYIPHYLVFNFMNFGSGICMFWLITDYLLCTASVYINVLISYDRYSQVSNV 120
QY 121 SYRAQHTGIMKIYQAVVAWILAFVNGPMLASDKNSTNTKDCRGFVTEWILIT 180
DB 121 SYRTQHTGIMKIYQAVVAWILAFVNGPMLASDKNSTNTKDCRGFVTEWILIT 180
QY 121 SYRTQHTGIMKIYQAVVAWILAFVNGPMLASDKNSTNTKDCRGFVTEWILIT 178
DB 121 SYRTQHTGIMKIYQAVVAWILAFVNGPMLASDKNSTNTKDCRGFVTEWILIT 178
QY 191 MLLEFLLPVISVAYENVVOIYVSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIVPILVAVFNMNIYVSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 238
QY 241 PGLKESAAHSRSESPPRKSSIIIVSLRTHMNSSITAFKVGSPWRSSEALRQREYAEILRG 300
DB 239 SASTEVPAFSPHSEQRQRKSSLMFSSRTKMSNTIAKMGSPQSDSVALHQREHVELIRA 298
QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYIAFLQWENSVNPLY 360
DB 299 RELAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYIAFLQWENSVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NOSVSS 391
DB 359 PLCHRRFQKAFWKILCVTKWPAISO-NOSVSS 390
RESULT 2
ID HH3R HUMAN STANDARD; PRT; 445 AA.
AC Q9Y5N1; Q9GZX2; Q9H4K8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
GN HH3 OR GPCR97.
OS Homo sapiens (Human).

```

-!- FUNCTION: The H3 subclass of histamine receptors could mediate the
histamine signals in CNS and peripheral nervous system. Signals
through the inhibition of adenylyl cyclase and displays high
constitutive activity (spontaneous activity in the absence of
agonist). Agonist stimulation of isoform 3 neither modified
adenylyl cyclase activity nor induced intracellular calcium
mobilization.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=Q9Y5N1-1; Sequence=Displayed;
Name=2;
IsoId=Q9Y5N1-2; Sequence=VSP_001886;
Name=3; Synonyms=H3S;
IsoId=Q9Y5N1-3; Sequence=VSP_001885;
Name=4;
IsoId=Q9Y5N1-4; Sequence=VSP_001881;
Name=5;
IsoId=Q9Y5N1-5; Sequence=VSP_001882;
Name=6;
IsoId=Q9Y5N1-6; Sequence=VSP_001883;
Name=7;
IsoId=Q9Y5N1-7; Sequence=VSP_001884;

-!- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the
greatest expression in the thalamus and caudate nucleus. The
various isoforms are mainly coexpressed in brain, but their
relative expression level varies in a region-specific manner.
Isoforms 3 and 7 are highly expressed in the thalamus, caudate
nucleus and cerebellum while isoforms 5 and 6 show a poor
expression. Isoforms 5 and 6 show a high expression in the
amygdala, substantia nigra, cerebral cortex and hypothalamus.
Isoform 7 is not found in hypothalamus or substantia nigra.

-!- DISEASE: Defects in HRH3 are a cause of Shy-drager syndrome
[MIM:146500]. This syndrome is characterized by orthostatic
hypotension, bladder and bowel incontinence, anhidrosis, iris
atrophy, anorexia, ataxia, rigidity and tremor.

-!- MISCELLANEOUS: Does not bind to cimetidine and triptolide. Shows
modest affinity for thioperamide, metit, N-alpha-methylhistamine
and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to
iodoproxyfan while isoforms 1 and 3 bind it with high affinity.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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or send an email to license@isb-sib.ch).

EMBL; AF140538; RAD38151.1; -
EMBL; AC045369; BAB20090.1; -
EMBL; AB019000; BAB17030.1; -
EMBL; AJ296652; CACS1025.1; -
EMBL; AJ278250; CAC39434.1; -
EMBL; AL078633; CAC04014.1; -
EMBL; AF363791; AAK50040.1; -
GeneW; HGNC:5184; HRH3.
MIM; 604525; -
MIM; 146500; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004969; F:histamine receptor activity; TAS.
GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS
GO; GO:0007269; P:neurotransmitter secretion; TAS.
InterPro; IPR000276; GPCR_Rhodopsin.
InterPro; IPR003980; H3_receptor.
Pfam; PF00001; 7tm.1; -
PRINTS; PR00237; GPCRHDOPSN.
PRINTS; PR01471; HISTAMINSH3R.
PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1.1; 1.
PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1.1; 1.

```


FT	TRANSMEM	399	419	POTENTIAL.
FT	DOMAIN	420	445	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	20	24	POLY-ALA.
FT	CARBOHYD	11	11	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	276	305	Missing (in isoform Short).
FT				/FTid=VSP_001880.
SQ	SEQUENCE	445 AA; 48734 MW; BAE206A3887189A0 CRC64;		

Query Match		35.2%;	Score 721;	DB 1;	Length 445;
Best Local Similarity		39.8%;	Pred. No. 8.2e-42;		
Matches 162;		Conservative 54;	Mismatches 133;	Indels 58;	Gaps 9;

QY	18	LAFIMSSFAFALMGVNAVVIILAFVVDRLMRHRSYFFFLNLAIISDFLVGLGISIPLYIPHL	77
DB	38	LAALMALILVATVLGNALWMLAFVADSLRTQNNFFLLNLAIISDFLVGVFCIPLYVPVL	97
QY	78	F-NNNFGSGICFMWLTIDYLCTASVNVILISYDRYQSUNAVSYRAOHTGIMKIVAQM	136
DB	98	TGRWTFGRGLCKLMDVDYLCTSSVFNILISYDRFLSVTRAVSYRAOQGDTRRVRKM	157
QY	137	VAVMILAFLVNPGMILASDSWK-----NSTNTKCEPGFVTEWILITITMLLEFLLPVIS	191
DB	158	VLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWFLTASTLBEFFTFELS	214
QY	192	VAYFNVQIY-----	214
DB	215	VTFFNLGIYLIQRRTRLRLDGGAREAGDPDLEPAQSSPPPPGCGWPKGGQESMPL	274
QY	215	HA-GFSTTSSA-SGLHRAGVACRTSNPGLKESAAASHSESPPRKSSILVSLRTHNWS	272
DB	275	HRYGVGAGPGAGEALGGSGAAASPTSSSGSSSRGTERPR-----SLKRGSKPS	327
QY	273	ITAFKVGSPWRSEBALQRREYAEALLRGRKLARLAILLSAFALCWAPYCLGFTIVLSTYP	332
DB	328	ASSASLEKRMKWVSQISITOR--FLSRDQKVAKSLAIIVSIFGLCWAPYELLMIRACH	385
QY	333	RTERPKSVWSYIAFWLQFNWSFVNPFLYPLCHRRFQKAFKILCVTK	379
DB	386	GHCVP-DYWYETSEFWLLWANSVAVNPVLYPLCHYSFRFAFTKLCPQK	431

RESULT 4		
HH3R	RAT	
ID	HH3R RAT	STANDARD; PRT; 445 AA.
AC	QOYN6; QOYN7; QOYN8; QOYN9;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Histamine H3 receptor (HH3R).	
GN	HRH3.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=10116;	
RN	[1]	
RN	SEQUENCE FROM N.A. (ISOFORM 1).	
RP	TISSUE=Hypothalamus;	
RC	TISSUE=Hypothalamus;	
RX	MEDLINE=20330707; PubMed=10869375;	
RA	Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;	
RT	"Cloning of rat histamine H3 receptor reveals distinct species	
RT	pharmacological profiles.;"	
RL	J. Pharmacol. Exp. Ther. 293:771-778(2000).	
RN	[2]	
RN	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
RP	TISSUE=Striatum;	
RC	TISSUE=Striatum;	
RX	MEDLINE=21016732; PubMed=11130725;	
RA	Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,	
RA	Stark H., Schumack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;	
RT	"High constitutive activity of native H3 receptors regulates histamine	
RT	neurons in brain.;"	
RL	Nature 408:860-864(2000).	
RN	[3]	
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).	


```

RESULT 6
ACM1_MACMU STANDARD; PRT; 460 AA.
ID ACM1_MACMU
AC P5649;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Muscarinic acetylcholine receptor M1.
GN CHRM1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens epithelium;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC -----
CC EMBL; AF026262; AAB95157.1; -.
CC HSP; P02699; IBOV.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRRHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC Pos-synaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 24
FT TRANSMEM 25 47
FT DOMAIN 48 61
FT TRANSMEM 62 82
FT DOMAIN 83 99
FT TRANSMEM 100 121
FT DOMAIN 122 141
FT TRANSMEM 142 164
FT DOMAIN 165 186
FT TRANSMEM 187 209
FT DOMAIN 210 366
FT TRANSMEM 367 387
FT DOMAIN 388 401
FT TRANSMEM 402 421
FT DOMAIN 422 460
FT CARBOHYD 2
FT CARBOHYD 12
FT DISULFID 98
FT MOD_RES 428
FT MOD_RES 451
FT MOD_RES 455
FT MOD_RES 457
FT MOD_RES 457
FT SEQUENCE 460 AA; 51432 MW; 1B19845C3BF79CA CRC64;
Query Match 20.4%; Score 418; DB 1; Length 460;
Best Local Similarity 27.8%; Pred. No. 2.3e-21;
Matches 123; Conservative 83; Mismatches 153; Indels 84; Gaps 19;

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Db 12 NITVLAPGKGPQVAFIGITTTGLSLATVTGNLLVLSFKVNTLKVNNVFLSLACAD 71
QY 62 FLVGLSIPLYIPIHVLIF-NMFGSGICMFWLLITDYLLCTASVYNNIVLISDYQSVGNV 120
Db 72 LIIGTFSMNLVITTYLLMGHWALGTACDLWLADYVNASVNNLLISFDYFVTRPL 131
QY 121 SYRAQHTGIMKIVAQWAV-WILAFVNGPMILASDSWKNSTWK-----DCPPGFVTEW 174
Db 132 SYRAKRT--PRRAALMIGLAWLWFLWAPAIL---FWQYLVGERTVLGAGCCYIQFLSQP 186
QY 175 YLITITMLLEFLLPVISVAYENVQIYWSLWKR-----RAL-----SRCPSHAGFTSS- 223
Db 187 IITFGTAMBAFVLPVTVMC-----TLIWRIVRETNARELAALQSGETPKGGGSSSSE 242
QY 224 ----SASGHLHR-AGVACRTSNP-----GLKESAAHSRHSPPRRKSSI 261
Db 243 RSQPGAEGSPETPPGRCRCRPPRLQAYSWKEDEEGSMESLTSSEGEPP--GSEV 300
QY 262 LVSL-----RTHNSSITAFKVGSWRSESA-----ALQRBYAEL 297
Db 301 VIKMPWVDPEAAPTQKPPRSPNTVKRPTKG---RDRAGKGQKPRGKEQLAKRTFSL 357
QY 298 LRGRKLARSILAILLSAPAIQWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLWNSFVNP 357
Db 358 VREKKAARTLSALLAFILTWPTNIMVIV-STFCXDCVPELW-ELGWLCYVNSTINP 415
QY 358 FLYPLCHRRFPQKAFKILCVTKW 380
Db 416 MCVALCNKAFRDTF-RLLLLCRW 437
RESULT 7
ACM5_MACMU STANDARD; PRT; 532 AA.
ID ACM5_MACMU
AC P56490;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Muscarinic acetylcholine receptor M5.
GN CHRM5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens epithelium;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC -----
CC EMBL; AF026264; AAB95159.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRRHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

```


Qy	121	SYRAQHTGIMKIVQAV--WILAFLVNGPMLASDWSKNSTNK-----DCEPGFVTEM	174
Db	132	SYRAKRT--PRRAIMTGLWLVFVWAPAIL---FWQYLVGERTVLGACQYIQLSQP	186
Qy	175	YLITITMLLEFLLPVISVAYENVOIYMSLWKR-----RAL-----SRCPFHAGFTTSSS	224
Db	187	IITGTAAAPYLPVTVMC-----TLYWKRIYETENRARELAALQGSFPGKGGSSSSE	242
Qy	225	AS-----CHLRHAGVACRT-----SNPGLKESAAASHSESPPRK	258
Db	243	RSQFGASGPETPPGRCR---CCRAPRLLOQAYSWKEEEDSGMESLTSSEGEPP--G	297
Qy	259	SSILVSL-----RTHMNSSITAFKVGSEFWRSESA-----ALRQREY	294
Db	298	SEVVIKPMVDPEAQATKPPRSPNTVKRPTKG---RDRAGKGQVDRKEQJAKRKT	354
Qy	295	AEILRGKRLARSAILLSAFAICWAPYCLFTFVILSTYPTRPKSVWYVIAFWLQWNSF	354
Db	355	FSLVKEKKAARTLSAILLAFILTWTPYINMLV-STFCKDCVPTLW-ELGYWLVCYNST	412
Qy	355	VNPPLYPLCHRRFOKAFWKILCVTKW	380
Db	413	INPCYALCNKAFRDTF-RLLLLCRW	437
RESULT 9			
ACMI_PIG	ID	ACMI_PIG	STANDARD; PRT; 460 AA.
AC	P04761;		
DT	DT 13-AUG-1987	(Rel. 05, Created)	
DT	DT 13-AUG-1987	(Rel. 05, Last sequence update)	
DT	DT 16-OCT-2001	(Rel. 40, Last annotation update)	
DE	DE Muscarinic acetylcholine receptor M1.		
GN	GN CHRM1.		
OS	OS Sus scrofa (Pig).		
OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=87014801; PubMed=3762692;		
RA	Kubo T., Fukuda K., Mikami A., Maeda A., Takahashi H., Mishina M.,		
RA	Haga T., Haga K., Ichiyama A., Kangawa K., Kojima M., Matsuo H.,		
RA	Hirose T., Numa S.		
RT	"cloning, sequencing and expression of complementary DNA encoding the		
RT	muscarinic acetylcholine receptor."		
RL	Nature 323:411-416(1986).		
CC	-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS		
CC	CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,		
CC	BREAKDOWN OF PHOSPHONOSTIDES & MODULATION OF POTASSIUM CHANNELS		
CC	THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI		
CC	TURNOVER.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; X04413; CAA28003.1; -		
DR	PIR; A24325; A24325.		
DR	HSSP; P02699; 1BOJ.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm.1; 1.		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PROSITE; PS00237; G PROTEIN RECEPT F1.1; 1.		
DR	PROSITE; PS00262; G PROTEIN RECEPT F1.2; 1.		

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KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 47 1 (POTENTIAL).
FT DOMAIN 48 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 2 (POTENTIAL).
FT DOMAIN 83 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 121 3 (POTENTIAL).
FT DOMAIN 122 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 164 4 (POTENTIAL).
FT DOMAIN 165 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 209 5 (POTENTIAL).
FT DOMAIN 210 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 6 (POTENTIAL).
FT DOMAIN 388 401 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 402 421 7 (POTENTIAL).
FT DOMAIN 422 460 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. .) (PROBABLE).
FT DISULFID 98 178 BY SIMILARITY.
FT MOD RES 428 428 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 451 451 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 455 455 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 457 457 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 460 AA; 51418 MW; C025C70EA43BC2AD CRC64;

Query Match 20.2%; Score 413; DB 1; Length 460;
Best Local Similarity 27.5%; Pred. No. 4.9e-21;
Matches 122; Conservative 83; Mismatches 154; Indels 84; Gaps 18;

QY 5 NSTGILPPAAQVPLAFL--MSSFAFALMGNAVIVLAFVVDRLNRHRSNYFFFLNLAISSD 61
DB 12 NITVLAPGKGWQVAFGIITGLLSLATVGNLLVLISFKVNTLKTNNYFLSLACAD 71

QY 62 FLVGLISIPLYPHVLP-NMNFSGGICMFWLITDYLLCTASVYINVLISYDRYQSVNAV 120
DB 72 LIIGTFSMNLYTTLVLMGHWALGTIACDLMLADYVNASVNMILLISFDYFVSVPRL 131

QY 121 SYRAHTGIMKIVQAVAV-NILAFVNGPMLASDSWKNSTNTK-----DCEPGFVTEM 174
DB 132 SYRAKRT--PRAALMIGLAWLVSVLWAPAL---FWOYIVGERTVLAGQCYQLFSQP 186

QY 175 YILITLMLLELLPVISVAYENVQVYLSLWKR-----RAL-----SRCFSGAGFTTSSS 224
DB 187 IITFGTAAAPVLPVTVMC-----TLYWKIYRETNARELAALQGETPGKGGSSSSSE 242

QY 225 AS-----CHLHRAGVACRT-----SNPGLKESAAGRHSSEPRK 258
DB 243 RSQPGAEGSPETPPGRCR---CCRAPRLQAYSWKEEEDGSMESLTSSEGEPE--G 297

QY 259 SSILVSL-----RTHMNSSITAFKVGSWRSAA-----LRQREYAE 297
DB 298 SEVVIKMPVDEAQAQAPKPPRSPENTVKRGRERAGKQKPRKEQAKRTTSL 357

QY 298 LRGRKLARSALLLSAFAICWAPYCLFTITVSTYPRTERPKSVWYSIAFWLQWNSFVNP 357
DB 358 VKEKAARTLSAILAFIVTWTPYINVLV-STFCCKDCVPELW-ELGWYLCVYNSTNP 415

QY 358 FLYPLCHRRFQKAFKWLICVTKW 380
DB 416 MCYALCNKAFRDTF-RLLILLCRW 437

RESULT 10
ACM5 RAT STANDARD; PRT; 531 AA.
AC P0831;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Muscarinic acetylcholine receptor M5.
GN CHRM5 OR CHRM-5.
OS Rattus norvegicus (Rat).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90166521; PubMed=3272174;
RA Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
RT "Cloning and expression of the human and rat m5 muscarinic
RT acetylcholine receptor genes.";
RL Neuron 1:403-410(1988).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=89214170; PubMed=2540186;
RA Liao C.-F., Themmen A.P.N., Joho R., Barberis C., Birnbaumer M.,
RA Birnbaumer L.;
RT "Molecular cloning and expression of a fifth muscarinic acetylcholine
RT receptor.";
RL J. Biol. Chem. 264:7328-7337(1989).
CC -1- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; M22926; AAA40658.1; -
DB EMBL; M22925; AAA41572.1; -
DB PIR; JT0531; JT0531.
DB InterPro; IPR000276; GPCR_Rhodopsn.
DB Pfam; PF00001; 7tm.1; 1.
DB PRINTS; PR00237; GPCRHDOPSN.
DB PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DB PROSITE; PS00262; G-PROTEIN RECP_F2_1; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 52 1 (POTENTIAL).
FT DOMAIN 53 65 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 66 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 125 3 (POTENTIAL).
FT DOMAIN 126 145 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 146 168 4 (POTENTIAL).
FT DOMAIN 169 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 213 5 (POTENTIAL).
FT DOMAIN 214 442 6 (POTENTIAL).
FT TRANSMEM 443 463 7 (POTENTIAL).
FT DOMAIN 464 477 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 478 497 7 (POTENTIAL).
FT DOMAIN 498 531 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 102 182 BY SIMILARITY.
FT MOD RES 500 500 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 504 504 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 531 AA; 60136 MW; 647CE0D5D75A2BB1 CRC64;

Query Match 20.0%; Score 410.5; DB 1; Length 531;
Best Local Similarity 24.6%; Pred. No. 8.3e-21;
Matches 122; Conservative 92; Mismatches 140; Indels 141; Gaps 15;

QY 16 VPLAFIMSSFAFALMGNAVIVLAFVVDRLNRHRSNYFFFLNLAISSDFLVGLISIPLYPH 75
DB 30 ITIAVTVAVSLMTVIGNVLMVWISFKVNSQLKTVNNYLLSLACADLIIGFMSMLTTY 89
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QY 76 VLF-WNFGSGICMPWLITDYLCTASVYNIIVLSIDRYQSVNAVSYRAQHT-----GIM 130
Db 90 ILMGRVWLGSLACDLALDVAASVNMVLLVISDFEYFETITPLTYRAKSTPKRAGIM 149
QY 131 KIVAQVAVVILAFVNGPMLIADSW-----KNSYTKCEPQFVTEWYILITITMLLEF 185
Db 150 IGLA-----WLVSFILWAPAILC---WQYLVGKRTVPPDECIQFLSEPTITFTGTAIAAF 201
QY 186 LLPVISVAYFNVQIYWSLWKR-----RALSRCP----- 213
Db 202 YIPSVWVITLYCIRYRETERKTKDLADLOGSDSVAEAKKREPAORTLLRSFFSPRSLA 261
QY 214 -----SHAGFTT---SSASGHLHRA-----GVACRTSNPGLKESA----- 247
Db 262 QRENOASWSRRSTSTGTQTLDSADWEKAEQVTTCSYPSEDEAKPTTDPVQ 321
QY 248 ---ASRHSSEPRKSSILVSLTHMSSI---TAFKVSFWRSESAALR----- 290
Db 322 MVYKSEAKESPGKESNTQETKTVNTRTENSVDYTPKFLSPAARHLKSQKCVAYKFR 381
QY 291 -----OREYAEALLGRKLAR 305
Db 382 LVVKADGTQETNGCRVKIMPCSPFVSKDPSTKGPDPNLSHQMTKKRVMVVKERAAQ 441
QY 306 SLAILLSAFAICWAPYCLFVITSTYRTERPKSVWYVSIAPFWLQWNSFVNPFLYPLCHR 365
Db 442 TLSAILLAFTITWTPYNIWLV-STFCDCKCPVTLWH-LGWLCYVNSTINPICYALCNR 499
QY 366 RFQKAPFKILCVTKM 380
Db 500 TFRKTF-KULLLCRW 513

RESULT 11

ACM3_PIG
ID ACM3_PIG STANDARD; PRT; 590 AA.
AC F1483;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muscarinic acetylcholine receptor M3.
GN CHRM3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296835; PubMed=3402600;
RA Akiba I., Kubo T., Maeda A., Bujo H., Nakai J., Mishina M., Numa S.;
RT "Primary structure of porcine muscarinic acetylcholine receptor III
and antagonist binding studies.";
RL FEBS Lett. 235:257-261(1988).
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; X12712; CAA31215.1; --
DR PIR; S01114; S01114.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

PRINTS: PR00237; GPCRHOOPS
PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 67
FT TRANSMEM 68 91
FT DOMAIN 92 104
FT TRANSMEM 105 125
FT DOMAIN 126 142
FT TRANSMEM 143 164
FT DOMAIN 165 184
FT TRANSMEM 185 207
FT DOMAIN 208 229
FT TRANSMEM 230 252
FT DOMAIN 253 492
FT TRANSMEM 493 513
FT DOMAIN 514 527
FT TRANSMEM 528 547
FT DOMAIN 548 590
FT CARBOHYD 6 6
FT CARBOHYD 7 7
FT CARBOHYD 8 8
FT CARBOHYD 15 15
FT CARBOHYD 41 41
FT CARBOHYD 48 48
FT CARBOHYD 53 53
FT DISULFID 141 221
SQ SEQUENCE 590 AA; 66077 MW; 9998D2A4802FD32A CRC64;
Query Match 20.0%; Score 410.5; DB 1; Length 590;
Best Local Similarity 24.8%; Pred. No. 9.1e-21;
Matches 125; Conservative 82; Mismatches 136; Indels 161; Gaps 16;
QY 18 LAFMSFAFAMVGNVAVILAFVDRNLRHRSNYFFFLNLAIISDFVLGSLIPLXIPHVL 77
Db 71 IAEFTGILAVTIIGNILVIVAFKVNKQKTVNNYFLLSLACADLLIGVSMMLFTYII 130
QY 78 FN-WNFGSGICMPWLITDYLCTASVYNIIVLSIDRYQSVNAVSYRAQHT-----GIMKI 132
Db 131 MNRWALGNLACDLWLSIDVVASNASVMNLLVISDFYFSITRPLTYRAKSTPKRAGVIM 190
QY 133 VQAVVAVVILAFVNGPMLIADSWKNSVNTKDCBPG-----FVTEWYILITITMLLEFL 187
Db 191 LA-----WVISFILWAPAIL---FWQYFVGKRTVPPDECIQFLSEPTITFTGTAIAAFY 242
QY 188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGF---STTSSASGHLHRAAGVACRTSNPGLKE 245
Db 243 PVITMTI---LYWRIYKETE-KRIKELAGLOASGTEAEAFVHPTGSSRSCSYELOQ 297
QY 246 SAASR-----HSES----- 254
Db 298 QSLKRSARKYGRCHFWFTTKGWKPSAEQMDQDSSSDSNMNNDAASLENSASSDEEDI 357
QY 255 ---PRKSSILVSLRTHM-----SSITAFKV----- 278
Db 358 GSETAIYSIVLKIPGHSTILNSTKLPSDNLQVPEELGTVDLERKASKLOAKQKMDDG 417
QY 279 GSFWR-----ESAA-----LRQ 291
Db 418 GSFQKSFSLPIQLESADVDTAKASDVNSVSGVKTATLPLSFKEATLAKRFAUKTRSIQTK 477
QY 292 RYAEALLGRKLARSLAILLSAFAICWAPYCLFVITSTYRTERPKSVWYVSIAPFWLQW 351
Db 478 RKRMSLIKEAKAQTLSAILLAFTITWTPYNIWLV-NTFDCSCPITYW-NLGWLCYI 535
QY 352 NSFVNPFLYPLCHRRFPQKAFWKIL 375
Db 536 NSTVNEVCYALCNKTKTFTTFRML 559

ACM1_RAT STANDARD; PRT; 450 AA.
P08482;
01-AUG-1998 (Rel. 08, Created)
01-AUG-1998 (Rel. 08, last sequence update)
28-FEB-2003 (Rel. 41, last annotation update)
Muscarinic acetylcholine receptor M1.
CHRM1 OR CHRM-1.
Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
MEDLINE=87263421; PubMed=3037705;
Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
genes.";
Science 237:527-532 (1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=92101806; PubMed=1759615;
Lai J., Smith T.B., Mei L., Ikeda M., Fujiwara Y., Gomez J.,
Halonen M., Roeseke W.R., Yamamura H.I.;
"The molecular properties of the M1 muscarinic receptor and its
regulation of cytosolic calcium in a eukaryotic gene expression
system.";
Adv. Exp. Med. Biol. 287:313-330 (1991).
[3]
MUTAGENESIS OF CYSTEINE RESIDUES.
MEDLINE=92283857; PubMed=1317867;
Savarese T.M., Wang C.-D., Fraser C.M.;
"Site-directed mutagenesis of the rat m1 muscarinic acetylcholine
receptor. Role of conserved cysteines in receptor function.";
J. Biol. Chem. 267:11439-11448 (1992).
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
TURNOVER.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; M16406; AAA00660.1; -;
EMBL; S73971; AAB20705.1; -;
PIR; A94518; A29514.
DR HSP; P02699; 1BOU.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 47 1 (POTENTIAL).
FT DOMAIN 48 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 2 (POTENTIAL).
FT DOMAIN 83 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 121 3 (POTENTIAL).
FT DOMAIN 122 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 164 4 (POTENTIAL).
FT DOMAIN 165 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 209 5 (POTENTIAL).
FT DOMAIN 210 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 6 (POTENTIAL).

DOMAIN 388 401 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 402 421 7 (POTENTIAL).
FT DOMAIN 422 460 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (PROBABLE).
FT DISULFID 98 178 PROBABLE.
FT MOD RES 428 428 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 451 451 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 455 455 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 457 457 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 460 AA; 51368 MW; 527573ED8FF7C317 CRC64;
Query Match 20.0%; Score 410; DB 1; Length 460;
Best Local Similarity 27.4%; Pred. No. 7.8e-21;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAVVVDRLRLRHSNYFFFLNLAISD 61
DB 12 NITVLAFGKGPQVAFIGITGLLSLATVGNLVLVLSFKVNTKVTNNYFLLSLACAD 71
QY 62 FLVGLISIPLYIPHLF-NMNFSGIGCMFWLITDYLCTASVYNIIVLISYDQYOSVNAV 120
DB 72 LIIGTFSNLYTYLLMGHMGALGTACDLWLALDYVNASVNMNLLISFDRIYSVTRPL 131
QY 121 SYRAQHTGIMKIVQMVAV-WILAFVNGPMLASDSWKNSTNK-----DCEPGFVTEW 174
DB 132 SYRAKRT--PRRAALMIGLAWLVSVFWLWAPAIL---FWQYLVGERTVLAGQCYIOFLSOP 186
QY 175 YLITITMLLEFLPLVISVAYENVOLYMSLWKR-----RAL-----SRCPSHAGFTTSSS 224
DB 187 IITGTAAAFYLPVTVMC-----TLWRIYRETNARELAALQSETPGKGGSSSSE 242
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAASHSSSPRRK 258
DB 243 RSQPAEGSPSPGRCR---CCRAPLLQAYSWEKEEEDGSMESLTSSESEP--G 297
QY 259 SSILVSL-----RTHMNSITAFKVGSPWRSSEA-----ALRQREY 294
DB 298 SEVVIKMPWVDSQAQPTKQPPKSPNTVKRPTKKG---RDRGGKQKPRGKEQLAKRKT 354
QY 295 AELLGRKLARSLAIIILSAFAICWAPYCLFTITVLSTYRTERPKSVWYSIAFWLQWNSF 354
DB 355 FSLVKEKKAARLSAILLAFLITWPNIMVLV-STFKDCVCPETLM-ELGYWLCYVNST 412
QY 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
DB 413 VNPMCYALCNKAFRDTE-RLLLLCRW 437
RESULT 13
ACM3_BOVIN STANDARD; PRT; 590 AA.
ID ACM3_BOVIN STANDARD; PRT; 590 AA.
AC P41984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Muscarinic acetylcholine receptor M3.
GN CHRM3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94339178; PubMed=8061048;
RA Lee P.H., Hodges P.K., Glickman F., Chang K.J.;
RT "Cloning and expression of a cDNA encoding bovine muscarinic
acetylcholine m3 receptor.";
RL Biochim. Biophys. Acta 1223:151-154 (1994).
RN [2]
RP SEQUENCE OF 327-467 FROM N.A.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:06:02 ; Search time 44 Seconds
(without alignments)
2803.809 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 2048
Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2035	99.4	391	11 Q91ZY2	Q91zy2 mus musculus
2	1745	85.2	391	11 Q91ZY1	Q91zy1 rattus norv
3	1372.5	67.0	390	4 Q96LD9	Q96ld9 homo sapien
4	1311.5	64.0	390	6 Q8MNV9	Q8mrv9 sus scrofa
5	1238	60.4	389	11 Q91ZY3	Q91zy3 cavia porce
6	718.5	35.1	445	6 Q865E1	Q865el macaca mula
7	665.5	32.5	365	4 Q8WY01	Q8wy01 homo sapien
8	665.5	32.5	373	4 Q8WY01	Q8wy01 homo sapien
9	492.5	24.0	301	4 Q8WY00	Q8wy00 homo sapien
10	492.5	24.0	309	4 Q8WY00	Q8wy00 homo sapien
11	415.5	20.3	530	11 Q8VH24	Q8vh24 cavia porce
12	413	20.2	454	4 Q96RH1	Q96rch1 homo sapien
13	410	20.0	460	11 Q8BJN3	Q8bjn3 mus musculus
14	410	20.0	587	11 Q8VH26	Q8vh26 cavia porce
15	406.5	19.8	532	4 Q81VW0	Q81vw0 homo sapien
16	406	19.8	490	13 Q7T286	Q7t286 brachydanio

17	405.5	19.8	200	4 Q8NI50	Q8ni50 homo sapien
18	405	19.8	458	11 Q8VH28	Q8vh28 cavia porce
19	402.5	19.7	564	4 Q96RG9	Q96rg9 homo sapien
20	401.5	19.6	528	13 Q9PTF6	Q9ptf6 gallus gall
21	401.5	19.6	532	11 Q920H4	Q920h4 mus musculus
22	393.5	19.2	518	6 Q9MYI8	Q9myi8 oryctolagus
23	392.5	19.2	400	6 Q8MKJ0	Q8mkj0 cebus apell
24	391	19.1	488	11 Q91V49	Q91v49 rattus norv
25	390.5	19.1	147	6 Q865E3	Q865e3 canis famil
26	390	19.0	571	6 Q9TWM9	Q9ttm9 sus scrofa
27	389.5	19.0	459	11 Q8CGI5	Q8cgl5 mus musculus
28	389.5	19.0	487	6 Q9N2B1	Q9n2b1 gorilla gor
29	389.5	19.0	487	6 Q9N2B0	Q9n2b0 pongo pygma
30	389.5	19.0	515	11 Q9DBL0	Q9db10 mus musculus
31	389	19.0	488	11 Q91V66	Q91v66 rattus norv
32	388.5	19.0	495	13 Q801M4	Q801m4 brachydanio
33	386.5	18.9	487	6 Q9N2B2	Q9n2b2 pan troglod
34	384.5	18.8	399	5 Q9NG02	Q9ng02 apis mellif
35	384	18.8	477	11 Q8VH25	Q8vh25 cavia porce
36	383.5	18.7	559	11 Q9QW71	Q9qw71 rattus sp.
37	382.5	18.7	466	11 Q8VH27	Q8vh27 cavia porce
38	382	18.7	399	4 Q13167	Q13167 homo sapien
39	382	18.7	474	4 Q96RG8	Q96rg8 homo sapien
40	381	18.6	415	13 Q8JG69	Q8jg69 brachydanio
41	380.5	18.6	456	4 Q96RH0	Q96rh0 homo sapien
42	380.5	18.6	506	5 Q8IS44	Q8is44 drosophila
43	378	18.5	461	5 Q8IS43	Q8is43 drosophila
44	376.5	18.4	410	5 Q86GT6	Q86gt6 caenorhabdi
45	376.5	18.4	422	5 Q8T3C1	Q8t3c1 caenorhabdi

ALIGNMENTS

RESULT 1

Q91ZY2 Q91ZY2 PRELIMINARY; PRT; 391 AA.
AC Q91ZY2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Histamine H4 receptor.
GN HRR4.
OS Mus musculus (Mouse).
OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
RT suggests substantial species variation."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF358859; AAK97380.1; -;
DR MGD; MGI:2429635; Hrh4.
DR GO; GO:0005887; C:Integral to plasma membrane; IC.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0004969; F:histamine receptor activity; IDA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008102; Histamine_H4.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00362; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;
Query Match 99.4%; Score 2035; DB 11; Length 391;
Best Local Similarity 99.7%; Pred. No. 1.7e-169;

Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60
 Db 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120
 Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120

Qy 121 SYRAQHTGIMKIVQAVAVILAFVNGPMLASDSWKNSTNTKDCBGFVTEWYILIT 180
 Db 121 SYRAQHTGIMKIVQAVAVILAFVNGPMLASDSWKNSTNTKDCBGFVTEWYILIT 180

Qy 181 MLEFLPLPVIISVAYFNVQIYWSLWKRRALSRCPHAGFSTSSASGHLHAGVACRTSN 240
 Db 181 MLEFLPLPVIISVAYFNVQIYWSLWKRRALSRCPHAGFSTSSASGHLHAGVACRTSN 240

Qy 241 PGLKESAAHRSSEPRRKSSILVSRTHMNSSITAFKVGSWRSAAALRQREYAEALLRG 300
 Db 241 PGLKESAAHRSSEPRRKSSILVSRTHMNSSITAFKVGSWRSAAALRQREYAEALLRG 300

Qy 301 RKLARSALILLSAFAICWAPYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFY 360
 Db 301 RKLARSALILLSAFAICWAPYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFY 360

Qy 361 PLCHRRFOKAFWKILCVTKWPALSONQSVSS 391
 Db 361 PLCHRRFOKAFWKILCVTKWPALSONQSVSS 391

RESULT 2

Q91ZY1 ID Q91ZY1 PRELIMINARY; PRT; 391 AA.

AC Q91ZY1; (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)

DE Histamine H4 receptor.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;

RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation."

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL; AF358860; AAK97381.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsin.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCR RHODOPSIN.

DR PRINTS; PR01726; HISTAMINEH4.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.

DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Receptor; Transmembrane.

SK SEQUENCE 391 AA; 44023 MW; C707BA639CFED41 CRC64;

Query Match 85.2%; Score 1745; DB 11; Length 391;

Best Local Similarity 84.9%; Pred. No. 3.6e-144;

Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60
 Db 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60

Db 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120
 Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120

Qy 121 SYRAQHTGIMKIVQAVAVILAFVNGPMLASDSWKNSTNTKDCBGFVTEWYILIT 180
 Db 121 SYRAQHTGIMKIVQAVAVILAFVNGPMLASDSWKNSTNTKDCBGFVTEWYILIT 180

Qy 181 MLEFLPLPVIISVAYFNVQIYWSLWKRRALSRCPHAGFSTSSASGHLHAGVACRTSN 240
 Db 181 MLEFLPLPVIISVAYFNVQIYWSLWKRRALSRCPHAGFSTSSASGHLHAGVACRTSN 240

Qy 241 PGLKESAAHRSSEPRRKSSILVSRTHMNSSITAFKVGSWRSAAALRQREYAEALLRG 300
 Db 241 PGLKESAAHRSSEPRRKSSILVSRTHMNSSITAFKVGSWRSAAALRQREYAEALLRG 300

Qy 301 RKLARSALILLSAFAICWAPYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFY 360
 Db 301 RKLARSALILLSAFAICWAPYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFY 360

Qy 361 PLCHRRFOKAFWKILCVTKWPALSONQSVSS 391
 Db 361 PLCHRRFOKAFWKILCVTKWPALSONQSVSS 391

RESULT 3

Q96LD9 ID Q96LD9 PRELIMINARY; PRT; 390 AA.

AC Q96LD9; (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)

DE Histamine receptor H4.

GN H4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC Nguyen T., George S.R., Lee D.K., Cheng R., Lynch K.R., O'Dowd B.F.;

RT "Discovery of H4, a Novel Histamine Receptor."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL; AY008280; AAL09297.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR Rhodopsin.

DR InterPro; IPR008102; Histamine_H4.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCR RHODOPSIN.

DR PRINTS; PR01726; HISTAMINEH4.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.

DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Receptor; Transmembrane.

SK SEQUENCE 390 AA; 44469 MW; CC82B5030D216C66 CRC64;

Query Match 67.0%; Score 1372.5; DB 4; Length 390;

Best Local Similarity 68.1%; Pred. No. 1.3e-111;

Matches 267; Conservative 41; Mismatches 81; Indels 3; Gaps 2;

Qy 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60
 Db 1 MSENSTGILPPAAQVPLAFMSFAFAMVGNVAVILAFVDRNLHRSNYFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120
 Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120


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QY 121 SYRAQHTGIMKIVAQMVAVIILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILIT 180
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 SYRTQHTGVKIVTLVAVVAVLAFVNGPMILVSEWDEGS--ECEPGFSEWYILAIT 178
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 MLLEFLLPVISVAVFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 SFLEFVIVPILVAVFNNIYWSLWKRDHLSCQSHPLGTAVSSNICGHSFRGLSSRSL 238
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 241 PGLKESAAASRHSERPRKSSILVSLRTHMNSITAFKVGSPWRSESAALRQREYAEILL 300
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 SASTEVPAFSEHQRRKSSLMFSRTKQNSNTTASKMGSPSQSDSVALHQREHYELLRA 298
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 301 RKLARSAILLSAFAICWAPYCLFTVILSTYPRTERPKSVWYSIAFWLQWNSFNPELY 360
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 RRLAKSAILLGVAFCWAPYSLFTVILSFYSSATGPKSVWYRIAFWLOWNSFNPELY 358
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 PLCHRRFOKAFWKILCVTKWPALSQ--NOSVSS 391
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 PLCHRRFOKAFKIFCIKKQPLPSQHSRSVSS 390
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 4
Q8WNV9 PRELIMINARY; PRT; 390 AA.
ID Q8WNV9
AC Q8WNV9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB053300; BAB83078.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;
Query Match 64.0%; Score 1311.5; DB 6; Length 390;
Best Local Similarity 65.9%; Pred. No. 2.7e-106;
Matches 299; Conservative 33; Mismatches 96; Indels 5; Gaps 3;
QY 1 MSERN--STGILPPAAQVPLAFMSSFAFAIMVGNVAVILAFVVDNRHRSNYFFNLIA 58
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MSAINDTNTPLNTRIALAFMLSLALVIMLGNAVILAFVVDNRHRSNYFFNLIA 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 59 ISDFVLGLISIPLYIPHLVFNWNGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSN 118
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ISDFVGVISIPLYIPHTLFKWLKLEONICAFWLIIDYLLCTASVYNIIVLSYDRYQSVSN 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 AVSYRAQHTGIMKIVAQMVAVIILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILIT 178
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 AVSYRTQHTGILKIVALMVGVMVILAFVHGPVILVSEAMKQ--GKQDCPFGFLKEWYVLA 178
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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QY 179 ITMLLEFLLPVISVAVFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRT 238
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 ITLFEFLAPVLLVAYFNLXIYWSLWKRGHLSRCQSHCGLTPVSSGWSGHSRCLGFSRT 238
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 SNPGLKESAAASRHSERPRKSSILVSLRTHMNSITAFKVGSPWRSESAALRQREYAEILL 298
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 SLSDPKKAAASLSHSEPRKSKTLWFSLRTRM--SSLTASNKGLFSDSDSLAHQKHELELL 297
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 299 RGRKLARSAILLSAFAICWAPYCLFTVILSTYPRTERPKSVWYSIAFWLQWNSFNPELY 358
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 298 RARLARSAILLGVAFCWAPYSLFTVILSTYPRTERPKSVWYSIAFWLQWNSFNPELY 357
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 359 LYPCLCHRRFOKAFWKILCVTKWPALSQ--NOSVSS 391
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 358 LYPCLCHRRFOKAFKIFCIKKQSTLSHNRSTSS 390
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 5
Q91ZY3 PRELIMINARY; PRT; 389 AA.
ID Q91ZY3
AC Q91ZY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
RT suggests substantial species variation.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF358858; AAK93739.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 389 AA; 44511 MW; 51AF32FD6F1C3B4F CRC64;
Query Match 60.4%; Score 1238; DB 11; Length 389;
Best Local Similarity 62.5%; Pred. No. 7e-100;
Matches 245; Conservative 43; Mismatches 100; Indels 4; Gaps 3;
QY 1 MSERNSTGILPPAAQVPLAFMSSFAFAIMVGNVAVILAFVVDNRHRSNYFFNLIAIS 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MLANNST-IALTSTIKSLTFLMSLLAIAIMLGNAVILAFVVDNRHRSNYFFNLIAIA 59
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 DFLVGLISIPLYIPHLVFNWNGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSN 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 DFFVGAIALPLXIIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSN 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 SYRAQHTGIMKIVAQMVAVIILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILITIT 180
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 WYEAQSGTGMKIVATQMVAVIIFSMINGPMILISDSWQNSTT--ECEPGFLKKWYFALPT 177
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 MLLEFLLPVISVAVFNVQIYWSLWKRRALSRCPSHAGF--STTSSASGHLHRAGVACRTS 239
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 178 SLLEFLIPILLVAYFSAHIYWSLWKREKLSRCLSHVPLPSDSSSDHGHSCRPDPSRAT 237
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 240 NPLKESAAASRHSERPRKSSILVSLRTHMNSITAFKVGSPWRSESAALRQREYAEILL 299
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```



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QY 311 LSFAICWAPYCLFTIVLSTYPTERPKSVVYSIAFWLQWNSFVNPFLYPLCHRRFOKA 370
Db 284 VSIFGLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRA 342
QY 371 FWKILCVTK 379
Db 343 FTKLLCPQK 351

RESULT 8
Q8WXZ9 PRELIMINARY; PRT; 373 AA.
AC Q8WXZ9
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 4.
GN HRH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Bursstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321913; AAL71914.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002276; GPCR Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR InterPro; IPR003980; H3 receptor.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 373 AA; 41570 MW; FAE9DFC5C3AF4DE9 CRC64;

Query Match 32.5%; Score 665.5; DB 4; Length 373;
Best Local Similarity 40.1%; Pred. No. 6.9e-50;
Matches 148; Conservative 46; Mismatches 114; Indels 61; Gaps 8;

QY 18 LAFLMSSFAFAIMVGNVAVILAFVVDRLNRHRSNYFFLNLAISDFLVGLISIPLYIPIHVL 77
Db 37 LAALMALLIVATVGLNALVMAFVADSSLRTONNFFLNLAISDFLVGAFCIPLYVYVYL 96
QY 78 F-NNFGSGICMFWLITDYLLCTASVYINVLISYDRYQSVSNVSVYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVDVYLLCTSSAFNLVLSYDRFLSVTRAVSVYRAQGTTRAVRQM 156
QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPGVFTWYILITIMLLEFLLPVIS 191
Db 157 LLVWVLAFLLYGPAFL--SWEYLSGGSSIPBGHCYAEFFYNWYFLITASTLEFFTFPLS 213
QY 192 VAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACKTSNPGLKESASRH 251
Db 214 VTFFNLISVLNQRTRL-----RLDGEAAAGPEPPPPQSP 252
QY 252 SSSPRKSSILVSLRTHMNSSITAFKVGFWRSSEAALEQREYAEILL-RGRKLARSALTL 310
Db 253 PPPP-----GCW-----GCWQKHGGEAMPLHRVAKSLAVI 283
QY 311 LSFAICWAPYCLFTIVLSTYPTERPKSVVYSIAFWLQWNSFVNPFLYPLCHRRFOKA 370
Db 284 VSIFGLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRA 342
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QY 371 FWKILCVTK 379
Db 343 FTKLLCPQK 351

RESULT 9
Q8WY00 PRELIMINARY; PRT; 301 AA.
AC Q8WY00;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 3.
GN HRH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Bursstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321912; AAL71913.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002276; GPCR Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR InterPro; IPR003980; H3 receptor.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;

Query Match 24.0%; Score 492.5; DB 4; Length 301;
Best Local Similarity 50.5%; Pred. No. 6.9e-35;
Matches 100; Conservative 30; Mismatches 59; Indels 9; Gaps 3;

QY 18 LAFLMSSFAFAIMVGNVAVILAFVVDRLNRHRSNYFFLNLAISDFLVGLISIPLYIPIHVL 77
Db 37 LAALMALLIVATVGLNALVMAFVADSSLRTONNFFLNLAISDFLVGAFCIPLYVYVYL 96
QY 78 F-NNFGSGICMFWLITDYLLCTASVYINVLISYDRYQSVSNVSVYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVDVYLLCTSSAFNLVLSYDRFLSVTRAVSVYRAQGTTRAVRQM 156
QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPGVFTWYILITIMLLEFLLPVIS 191
Db 157 LLVWVLAFLLYGPAFL--SWEYLSGGSSIPBGHCYAEFFYNWYFLITASTLEFFTFPLS 213
QY 192 VAYFNVQIYWSLWKRRAL 209
Db 214 VTFFNLISVLNQRTRL 231

RESULT 10
Q8NI49 PRELIMINARY; PRT; 309 AA.
AC Q8NI49;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 6.
GN HRH3.
```



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DR GO:0016021; C: integral to membrane; IEA.
DR GO:0004872; F: receptor activity; IEA.
DR GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE: PS0262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 454 AA; 50748 MW; 68D02A29898C8D92 CRC64;

Query Match 20.2%; Score 413; DB 4; Length 454;
Best Local Similarity 27.4%; Pred. No. 9.9e-28;
Matches 122; Conservative 84; Mismatches 150; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL---MSSFAFAMVGNNAVILAFVVDRLNRHSNYFFNLALISD 61
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 12 NITVLAFGKGPQVAFIGITTTGLSLATVTGNLLVLISFKVNTLKTWNVYFLLSLACAD 71
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 FLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISDYRQSVSNV 120
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 LIIGTFSMNLYTYLLMGHWALGTACDLMLALDYVASNASVMNLLISFDYFVTRPL 131
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 SYRAQHTGIMKIVAQVAV-WILAFVNGPMILASDSWKSTNTK-----DCEPGFVTEW 174
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQYLVGERTVLACQYIQFLSQP 186
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 YILITMLLEFLPLVISVAVFNVQIYWSLWK-----RAL-----SRCPHAGFTSTSS 224
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 IITFGTAAAFYLPVTVMC-----TLYWKIYRETNARELAALQGSPTPKGGSGSSSE 242
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAHSRHSERPRK 258
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 RSQPGAEGSPETPPGCCR---CCRAPRLQAYSWKEEEDSGMESLTSSEGEEP--G 297
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 259 SSILVSL-----RTHMNSITAFKVGFWRSESA-----ALRQREY 294
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 SEVVIKMPVDPPEAQAFTKPPRSSPTVVKRTKKG---RDRAGKQKPRGKQLAKRKT 354
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSYPTERPKSVWYSYAFWLQWNSF 354
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 FSLVKEKKAARTLSAILLAFILTWTPYINMLV-STFKDCVPETLW-ELGYWLCYVNST 412
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 413 INPMCVALCNKAPRDTF-RLLLLCRW 437
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
Q8BJN3 PRELIMINARY; PRT; 460 AA.
AC Q8BJN3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Muscarinic acetylcholine receptor M1.
GN CHRM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Striatum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK081248; BAC38175.1; -.
DR MGD; MGI:88396; Chrm1.

DR GO:0016021; C: integral to membrane; IEA.
DR GO:0004872; F: receptor activity; IEA.
DR GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE: PS0262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 454 AA; 50748 MW; 68D02A29898C8D92 CRC64;

Query Match 20.0%; Score 410; DB 11; Length 460;
Best Local Similarity 27.4%; Pred. No. 1.8e-27;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL---MSSFAFAMVGNNAVILAFVVDRLNRHSNYFFNLALISD 61
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 12 NITVLAFGKGPQVAFIGITTTGLSLATVTGNLLVLISFKVNTLKTWNVYFLLSLACAD 71
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 FLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISDYRQSVSNV 120
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 LIIGTFSMNLYTYLLMGHWALGTACDLMLALDYVASNASVMNLLISFDYFVTRPL 131
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 SYRAQHTGIMKIVAQVAV-WILAFVNGPMILASDSWKSTNTK-----DCEPGFVTEW 174
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQYLVGERTVLACQYIQFLSQP 186
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 YILITMLLEFLPLVISVAVFNVQIYWSLWK-----RAL-----SRCPHAGFTSTSS 224
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 IITFGTAAAFYLPVTVMC-----TLYWKIYRETNARELAALQGSPTPKGGSGSSSE 242
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAHSRHSERPRK 258
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 RSQPGAEGSPETPPGCCR---CCRAPRLQAYSWKEEEDSGMESLTSSEGEEP--G 297
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 259 SSILVSL-----RTHMNSITAFKVGFWRSESA-----ALRQREY 294
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 SEVVIKMPVDPPEAQAFTKPPRSSPTVVKRTKKG---RDRAGKQKPRGKQLAKRKT 354
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSYPTERPKSVWYSYAFWLQWNSF 354
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 FSLVKEKKAARTLSAILLAFILTWTPYINMLV-STFKDCVPETLW-ELGYWLCYVNST 412
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 413 INPMCVALCNKAPRDTF-RLLLLCRW 437
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
Q8VH26 PRELIMINARY; PRT; 587 AA.
AC Q8VH26;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Muscarinic receptor 3.
GN GPM3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA So I., Yang D., Kim H., Min K., Kim S., Kim K., Park K., Choi K.,
RA Kim I.;
RT "Five subtypes of muscarinic receptors are expressed in gastric smooth
RT muscles of Guinea pig."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AY072060; AAL67911.1; -.
DR GO:0016021; C: integral to membrane; IEA.
DR GO:0004872; F: receptor activity; IEA.
DR GO:0001584; F: rhodopsin-like receptor activity; IEA.
```

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DR Pfam: PF000001; 7tm.1; 1.
DR PRINTS; PR00237; GFCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR KW Receptor.
SQ SEQUENCE      532 AA;  60085 MW;  6674707AlB493C67 CRC64;

Query Match              19.8%;   Score 406.5;   DB 4;   Length 532;
Best Local Similarity    25.1%;   Pred No. 4.4e-27;
Matches 124; Conservative 89; Mismatches 141; Indels 141; Gaps 16;

QY      16 VPLAFLMSSPAFAIMVGNNAVILLAFVDNRNLRHSNYFFNLALISDFLVGLIISPLYLPH 75
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      76 VLF-NNFNGGGICMFMLITDYLCTASVNIIVLISDYQSVSNAVSYRAOHT---GIM 130
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      91 ILMGRWALGSLACDLWLADLYDVASNASVMNLLVISFDRIYSITRPLTYTRAKRTPKRAGIM 150
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      131 KIVAQMVAWILAFVLNPGMILASDSW-----KNSTNTKDCPEGFVTEWYILTITMLEF 185
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      151 IGIA-----WLISFILWAPALIC--WQLVGKKTVPDLDECIQIFLSEPTITFGTAIAAF 202
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      186 LLPVISVAYFNVOIYWSLWKR-----RALSRCP----- 213
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      203 YIPVSVMTILYCRIYRETEKTKTDLADIQSDSVTKAEKKPAHRAUFRSLCRCPRLTA 262
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      214 ----SHAGFTT--SSASAGHLRHAG-----VACT-----SNPGLK 244
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      263 QRENQASWGSSRRSTSTTGPSQATGPSANWAKAEQLTTCSSYPSSSEDEDKPATDPVLQ 322
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      245 ESAASRSESPPRKSS-----ILVSURTHMNSSIT-----AFKVG 279
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      323 VYKSQKSGESGEFSAAETEEIFVKAETEKSDYDTPNYLLSPAAAHPRKSKCVAYKFR 382
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      280 SFWRSE-----SAALRQRYEALLRGKLAR 305
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      383 LVKADGNQNETNNGCHKVKIMPCPPFPVAKEPSTKGLNPENPQHMTKRVVLVGRKKAQ 442
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      306 SLAILLSAFAICWAPYCLFTVLVSTPYRTERPKSVWYSIAFWLOWNFNSVNPFLPLCHR 365
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      443 TLSAILLAFAITWTPIYNIMVLV-STFCDCKVPVTLWH-LGYWLCVNVSTNPICVALCNR 500
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      366 RFQKAFWKILCVTKW 380
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      501 TFRKTF-KMILLCRW 514
DB      :|::||::||::||::||::||::||::||::||::||::||::||::||::||

Search completed: October 1, 2004, 10:12:40
Job time : 48 secs

```

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: October 1, 2004, 10:13:10 ; Search time 125 Seconds
(without alignments)
883.809 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSNSTGILPPAAQVPLAF.....WKILCVTKWPAISQNSVSS 391

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : 1: A Geneseq_29Jan04.*
2: Geneseqp1980s.*
3: Geneseqp1990s.*
4: Geneseqp2000s.*
5: Geneseqp2001s.*
6: Geneseqp2002s.*
7: Geneseqp2003as.*
8: Geneseqp2003bs.*
9: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	379	96.9	391	5	AAM50565
2	33	8.4	391	5	AAM50566
3	32	8.2	389	5	AAM50567
4	21	5.4	73	4	AAG80931
5	21	5.4	73	5	ABG93749
6	21	5.4	357	6	ABG93749 Human G p
7	21	5.4	390	3	AAB2831
8	21	5.4	390	3	AAU71297
9	21	5.4	390	4	ABG62445
10	21	5.4	390	4	ABG64477
11	21	5.4	390	4	ABG64477 Human G p
12	21	5.4	390	4	AAM51410
13	21	5.4	390	4	ABG73622
14	21	5.4	390	5	AAM53050
15	21	5.4	390	5	ABP98629
16	21	5.4	390	5	ABP98629 Human his
17	21	5.4	390	5	ABP78276 Amino aci
18	21	5.4	390	5	AAM50564
19	21	5.4	390	5	AAU74906
20	21	5.4	390	6	ABG71960
21	21	5.4	390	6	ABU92265
22	21	5.4	390	6	ABP81727
23	21	5.4	390	6	ABP81727 Human his
24	21	5.4	390	6	AAB36417
25	21	5.4	391	5	AAM53052
26	21	5.4	392	5	AAM53053

26	21	5.4	441	5	ABE23411	Aae23411 Human G-p
27	21	5.4	592	4	ABG28404	Abg28404 Novel hum
28	21	5.4	592	4	ABG25785	Abg25785 Novel hum
29	14	3.6	336	6	AAE36414	Aae36414 Human H4
30	11	2.8	19	2	AAW92979	Aaw92979 Human mAC
31	11	2.8	19	2	AAG67833	Aag67833 Human mAC
32	11	2.8	19	2	AAG67840	Aag67840 Rat mACHR
33	11	2.8	19	6	ABG76408	Abg76408 Human mus
34	11	2.8	19	6	ABG76415	Abg76415 Rat musca
35	11	2.8	168	4	AAU25653	Aau25653 G protein
36	11	2.8	230	4	AAU27516	Aau27516 Human G-P
37	11	2.8	290	7	AAO29538	Aao29538 Human H3
38	11	2.8	293	7	AAO29537	Aao29537 Human H3
39	11	2.8	326	7	AAO29532	Aao29532 Human H3
40	11	2.8	329	7	AAO29531	Aao29531 Human H3
41	11	2.8	329	7	AAO29535	Aao29535 Human H3
42	11	2.8	340	4	AAB82911	Aab82911 Human his
43	11	2.8	351	4	AAG65581	Aag65581 Human his
44	11	2.8	365	4	AAG65580	Aag65580 Human his
45	11	2.8	365	7	AAO29528	Aao29528 Human H3

ALIGNMENTS

RESULT 1

AAM50565

ID AAM50565 standard; protein; 391 AA.

XX AC

XX AAM50565;

XX

DT 18-MAR-2002 (first entry)

XX

DE Mouse histamine H4 receptor.

XX

KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy.

XX

OS Mus musculus.

XX

PN WO200192485-A1.

XX

PD 06-DEC-2001.

XX

PF 22-FEB-2001; 2001WO-US005914.

XX

PR 31-MAY-2000; 2000US-0208260P.

XX

PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX

PI Lovenberg T, Liu C;

XX

DR WPI; 2002-114339/15.

XX

DR N-PSDB; AAI70981.

XX

CC New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

XX

PS Claim 13; Fig 5B; 92pp; English.

XX

CC The present sequence is that of a mouse histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful

CC for diagnosing, treating or preventing asthma, allergy, inflammation,
CC cardiovascular and cerebrovascular disorders, non-insulin dependent
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
CC the neuroendocrine system, stress and spasticity
XX
SQ Sequence 391 AA;
Query Match 96.9%; Score 379; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSENSTGILPPAAQVPLAFMSSFAFALMVGNAVWILAFVVDNLRHRSNYFFLNLAIS 60
Db 1 MSENSTGILPPAAQVPLAFMSSFAFALMVGNAVWILAFVVDNLRHRSNYFFLNLAIS 60
Qy 61 DFLVGLISIPLYIPHLVFNWFGSGICMFMLITDYLLCTASVYNIVLISYDRYQSVSNV 120
Db 61 DFLVGLISIPLYIPHLVFNWFGSGICMFMLITDYLLCTASVYNIVLISYDRYQSVSNV 120
Qy 121 SYRAQHTGIMKIVQAVWILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWILTIT 180
Db 121 SYRAQHTGIMKIVQAVWILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWILTIT 180
Qy 181 MLLRELLPVI SVAVFNVOIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 181 MLLRELLPVI SVAVFNVOIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Qy 241 POLKESAAARHSESPPRRKSSILVSLRTHMNGSITAFKVGSPWRSSAALRQREYAE LLRG 300
Db 241 POLKESAAARHSESPPRRKSSILVSLRTHMNGSITAFKVGSPWRSSAALRQREYAE LLRG 300
Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSWYSIAPWLQWNSFVNPFY 360
Db 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSWYSIAPWLQWNSFVNPFY 360
Qy 361 PLCHRRFOKAFWKILCVTK 379
Db 361 PLCHRRFOKAFWKILCVTK 379

RESULT 2
AAM50566
ID AAM50566 standard; protein; 391 AA.
XX AC AAM50566;
XX AC
XX 18-MAR-2002 (first entry)
XX Rat histamine H4 receptor.
XX
XX Histamine H4 receptor; rat; antiasthmatic; antiallergenic;
KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy.
XX
XX Rattus rattus.
XX
XX WO200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
DR N-PSDB; AAI70982.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.
XX Claim 13; Fig 6A; 92pp; English.
XX
CC The present sequence is that of a rat histamine receptor of the H4
CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA
CC library. The invention provides mammalian (human, mouse, rat and guinea
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC recombinant host cells that produce active recombinant protein. The
CC pharmacology of known histamine ligands is demonstrated. Mammalian
CC histamine H4 receptor may be used in gene therapy for the treatment of
CC diseases where it is beneficial to elevate mammalian histamine H4
CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the histamine H4 receptor. Such modulators may be useful
CC for diagnosing, treating or preventing asthma, allergy, inflammation,
CC cardiovascular and cerebrovascular disorders, non-insulin dependent
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
CC the neuroendocrine system, stress and spasticity
XX
SQ Sequence 391 AA;
Query Match 8.4%; Score 33; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 131 KIVAQWAVWILAFVNGPMLASDSWKNSTNT 163
Db 131 KIVAQWAVWILAFVNGPMLASDSWKNSTNT 163
RESULT 3
AAM50567
ID AAM50567 standard; protein; 389 AA.
XX AC AAM50567;
XX AC
XX 18-MAR-2002 (first entry)
XX Guinea pig histamine H4 receptor.
XX
XX Histamine H4 receptor; guinea pig; antiasthmatic; antiallergenic;
KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy.
XX
XX Cavia porcellus.
XX
XX WO200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
DR N-PSDB; AAI70983.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Claim 13; Fig 6C; 92pp; English.
XX
XX The present sequence is that of a guinea pig histamine receptor of the H4
XX subtype, as predicted from a cDNA clone isolated from a bone marrow
CC library. The invention provides mammalian (human, mouse, rat and guinea
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in

CC recombinant host cells that produce active recombinant protein. The
 CC pharmacology of known histamine ligands is demonstrated. Mammalian
 CC histamine H4 receptor may be used in gene therapy for the treatment of
 CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptor activity. Recombinant protein is useful for identifying
 CC modulators of the histamine H4 receptor. Such modulators may be useful
 CC for diagnosing, treating or preventing asthma, allergy, inflammation,
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
 CC the neuroendocrine system, stress and spasticity
 XX Sequence 389 AA;

Query Match 8.2%; Score 32; DB 5; Length 389;
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 89 FWLITDYLCTASVYNIVLISYDRYQSVSNV 120
 Db 88 FWLITDYLCTASVYNIVLISYDRYQSVSNV 119

RESULT 4
 AAG80931
 ID AAG80931 standard; protein; 73 AA.
 AC AAG80931;
 XX

DT 28-AUG-2001 (first entry)
 XX

DE Human nGPCR4.
 XX

XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective.
 XX

OS Homo sapiens.
 XX

XX WO200136473-A2.
 XX

PN 25-MAY-2001.
 XX

PD 16-NOV-2000; 2000WO-US031581.
 XX

PF 16-NOV-1999; 99US-0165838P.
 XX

PR 17-NOV-1999; 99US-0166071P.
 PR

PR 19-NOV-1999; 99US-0166678P.
 PR

PR 28-DEC-1999; 99US-0173396P.
 PR

PR 22-FEB-2000; 2000US-0184129P.
 PR

PR 28-FEB-2000; 2000US-0185421P.
 PR

PR 28-FEB-2000; 2000US-0185554P.
 PR

PR 02-MAR-2000; 2000US-0186530P.
 PR

PR 09-MAR-2000; 2000US-0186811P.
 PR

PR 17-MAR-2000; 2000US-0190310P.
 PR

PR 21-MAR-2000; 2000US-0190800P.
 PR

PR 20-APR-2000; 2000US-0198568P.
 PR

PR 02-MAY-2000; 2000US-0201190P.
 PR

PR 08-MAY-2000; 2000US-0203111P.
 PR

PR 25-MAY-2000; 2000US-0207094P.
 XX

XX (PHAA) PHARMACIA & UPJOHN CO.
 XX

XX Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
 PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RW;
 XX WPI; 2001-389826/41.
 XX

DR N-PSDB; AAH50971.
 XX

PT New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
 useful for diagnosing and treating e.g. schizophrenia.
 XX

PS Claim 37; Page 77; 261pp; English.
 XX

XX The present invention relates to novel G protein-coupled receptors
 (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
 one such G protein-coupled receptor. GPCRs are also known as seven
 transmembrane receptors and function in signal transduction. The nGPCRx
 coding sequences are useful for screening a human to diagnose a disorder
 affecting the brain or a genetic predisposition, specifically
 schizophrenia. nGPCRx are useful for identifying compounds useful for
 treating schizophrenia. Detection of nGPCRx in a sample is useful as a
 diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 metabolic and cardiovascular diseases, proliferative disorders and
 hormonal disorders. Modulators of nGPCRx activity have the utility for
 treating neurological disorders, including schizophrenia, ADHD/ADD
 (attention deficit-hyperactivity disorder/attention deficit disorder),
 and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 migraine and senile dementia. Additional disorders include inflammatory
 conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 disorders, cancers, respiratory ailments such as asthma, and inflammatory
 diseases e.g. inflammatory bowel disease
 XX

SQ Sequence 73 AA;
 XX

Query Match 5.4%; Score 21; DB 4; Length 73;
 Best Local Similarity 100.0%; Pred. No. 5.1e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113
 |||||

Db 31 TDYLLCTASVYNIVLISYDRY 51
 |||||

RESULT 5
 ABG93749

ID ABG93749 standard; protein; 73 AA.
 XX

AC ABG93749;
 XX

DT 26-NOV-2002 (first entry)
 XX

DE Human G protein-coupled receptor protein, beGPCR-seq4.
 XX

XX Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
 KW nG protein coupled receptor; communication; serpentine structure;
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
 KW genetic predisposition; brain; immune response; gene therapy;
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;
 KW Huntington's disease; dyskinesia; manic depression; stroke;
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
 KW tranquiliser.
 XX

OS Homo sapiens.
 XX

XX WO200264789-A1.
 XX

XX 22-AUG-2002.
 XX

XX 14-FEB-2001; 2001WO-US004641.
 XX

XX 14-FEB-2001; 2001WO-US004641.
 XX

XX (PHAA) PHARMACIA & UPJOHN CO.
 XX

XX Lind P, Parodi LA, Vogeli G, Wood LS;
 XX

XX WPI; 2002-674879/72.
 XX

DR N-PSDB; ABS70204.
XX
PT New nucleic acids and polypeptides of the nG protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.
XX
XX Example 1; Page 72; 244pp; English.
XX
XX The invention discloses an isolated human polypeptide, and encoding
XX nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
XX nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
XX communication between cells and their environment and are characterised
XX by a serpentine structure that passes through the cell membrane seven
XX times, hence the reason such receptors are sometimes called seven
XX transmembrane receptors (7TM). The polynucleotides and polypeptides are
XX useful for identifying an nGPCR allelic variant that correlates with a
XX mental disorder, for isolating an antibody that binds to an epitope of
XX the polypeptide, for identifying a compound that binds the polypeptide or
XX polynucleotide and/or modulates its biological activity, for screening a
XX human subject to diagnose a disorder, or a genetic predisposition to a
XX disorder, affecting the brain or a genetic disposition to the disorder,
XX for identifying compounds useful for the treatment of a mental disorder
XX and for identifying a compound useful as a modulator of binding between
XX nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
XX useful for inducing an immune response in a mammal. The nucleic acid or
XX polypeptide is particularly useful, using gene therapy, for treating e.g.
XX anxiety disorders, depression, bipolar disorder, schizophrenia,
XX Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
XX disease or Alzheimer's disease. The nucleic acid and polypeptide may also
XX be used for treating diabetes, inflammation or wounds. The sequences
XX presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also
XX referred to as beGPCRs) proteins
XX
XX Sequence 73 AA;
XX
Query Match 5.4%; Score 21; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 93 TDYLLCTASVNVNVLISYDRY 113
Db 31 TDYLLCTASVNVNVLISYDRY 51
XX
RESULT 6
AAE36415
ID AAE36415 standard; protein; 357 AA.
XX
AC AAE36415;
XX
XX 07-AUG-2003 (first entry)
XX
DE Human H4 receptor splice variant (H4c) protein.
XX
XX Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
XX atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
XX chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
XX rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
XX asthma; receptor; variant.
XX
XX Homo sapiens.
XX
XX WO2003020907-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027891.
XX
XX 31-AUG-2001; 2001US-0316762P.
XX
XX 13-NOV-2001; 2001US-0332697P.
XX
XX (MERI) MERCK & CO INC.

XX Gallagher MJ, Yates SL;
XX WPI; 2003-290186/28.
DR N-PSDB; AAD55124.
XX
XX Novel splice variants of human H4 histamine receptor, H4b and H4c, useful
XX for identifying agonists or antagonists of the receptor which are useful
XX for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
XX
XX Claim 21; Page 50-51; 31pp; English.
XX
XX The invention relates to splice variants of human H4 histamine receptor,
XX H4b and H4c. The invention is useful for identifying an agonist,
XX antagonist or inverse agonist of a mammalian histamine receptor. The
XX agonist, antagonist or inverse agonist of H4b and H4c is useful for
XX treating inflammation, asthma, allergy, atopic dermatitis, stroke,
XX myocardial infarction, migraine, chronic obstructive pulmonary disease
XX (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
XX disease, or psoriasis. The present sequence is human H4c protein
XX
XX Sequence 357 AA;
XX
Query Match 5.4%; Score 21; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 93 TDYLLCTASVNVNVLISYDRY 113
Db 93 TDYLLCTASVNVNVLISYDRY 113
XX
RESULT 7
AAB02831
ID AAB02831 standard; protein; 390 AA.
XX
AC AAB02831;
XX
XX 22-AUG-2000 (first entry)
XX
XX Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
XX
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical; mutant.
XX
XX Homo sapiens.
XX
XX WO200022131-A2.
XX
XX 20-APR-2000.
XX
XX 13-OCT-1999; 99WO-US024065.
XX
XX 13-OCT-1998; 98US-00170496.
XX
XX 12-NOV-1998; 98US-0108029P.
XX
XX 27-NOV-1998; 98US-0109213P.
XX
XX 16-FEB-1999; 98US-0110060P.
XX
XX 26-FEB-1999; 98US-0120416P.
XX
XX 12-MAR-1999; 98US-0121852P.
XX
XX 12-MAR-1999; 99US-0123944P.
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XX 12-MAR-1999; 99US-0123945P.
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XX 12-MAR-1999; 99US-0123946P.
XX
XX 12-MAR-1999; 99US-0123949P.
XX
XX 28-MAY-1999; 99US-0123951P.
XX
XX 28-MAY-1999; 99US-0136436P.
XX
XX 28-MAY-1999; 99US-0136437P.
XX
XX 28-MAY-1999; 99US-0136439P.
XX
XX 28-MAY-1999; 99US-0137127P.
XX
XX 28-MAY-1999; 99US-0137131P.
XX
XX 28-MAY-1999; 99US-0137567P.
XX
XX 29-JUN-1999; 99US-0141448P.
XX
XX 27-AUG-1999; 99US-0151114P.

PR	28-MAY-1999;	99US-0136436P.
PR	28-MAY-1999;	99US-0136437P.
PR	28-MAY-1999;	99US-0136439P.
PR	28-MAY-1999;	99US-0136567P.
PR	28-MAY-1999;	99US-0137127P.
PR	28-MAY-1999;	99US-0137131P.
PR	29-JUN-1999;	99US-0141448P.
PR	29-SEP-1999;	99US-0156555P.
PR	29-SEP-1999;	99US-0156633P.
PR	29-SEP-1999;	99US-0156634P.
PR	29-SEP-1999;	99US-0156653P.
PR	01-OCT-1999;	99US-0157280P.
PR	01-OCT-1999;	99US-0157281P.
PR	01-OCT-1999;	99US-0157282P.
PR	01-OCT-1999;	99US-0157293P.
PR	01-OCT-1999;	99US-0157294P.
PR	12-OCT-1999;	99US-00416760.
PR	12-OCT-1999;	99US-00417044.
XX	(AREN-) ARENA PHARM INC.	
PA	Chen R, Dang HT, Liaw CW, Lin I;	
PI		
XX		
DR	WPI; 2000-400068/34.	
DR	N-PSDB; AAD01124.	
XX		
PT	Novel human orphan G protein-coupled receptors and the encoding cDNAs for	
PT	use in the identification of G protein-coupled receptor agonists.	
XX		
PS	Claim 26; Page 60-61; 102pp; English.	
XX		
CC	The present amino acid sequence is the hRUP7, an endogenous human orphan	
CC	G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned	
CC	by RT-PCR using human peripheral leucocyte cDNA as template. The orphan	
CC	GPCR of the invention, like all GPCRs has seven transmembrane alpha	
CC	helices with an extracellular N-terminus and an intracellular C-terminus.	
CC	However, no endogenous ligands has yet been identified for the proteins	
CC	of the invention. The orphan GPCRs may be used in the identification of	
CC	their endogenous ligands, and to screen potential GPCR agonists and	
CC	antagonists for use as pharmaceutical agents. The proteins may also be	
CC	used in the study of GPCR-mediated signalling cascades, and to elucidate	
CC	their precise role in normal and diseased human conditions. Nucleic acid	
CC	encoding human orphan GPCRs may be used for tissue localisation	
CC	expression analysis to provide information about their function in	
CC	healthy and pathological states	
XX		
SQ	Sequence 390 AA;	
	Query Match	5.4%; Score 21; DB 3; Length 390;
	Best Local Similarity	100.0%; Pred. No. 2.6e-12;
	Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	93 TDYLLCTASVNIIVLSYDHY 113	
Dd	93 TDYLLCTASVNIIVLSYDHY 113	
RESULT 9		
AAB62445		
ID	AAB62445 standard; protein; 390 AA.	
XX		
AC	AAB62445;	
XX		
DT	09-JUL-2001 (first entry)	
XX		
DE	Human GPCR-like polypeptide, PFI-013.	
XX		
KW	G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;	
KW	antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;	
KW	osteopathic; neuroprotective; nootropic; dermatological; gynecological;	
XX	signal transduction.	
OS	Homo sapiens.	

XX PD 28-JUN-2001.
 XX XX
 XX PF 20-DEC-2000; 2000WO-JP009038.
 XX XX
 XX PR 20-DEC-1999; 99JP-00361687.
 XX XX
 XX PA (BANY) BANYU PHARM CO LTD.
 XX XX
 XX PI Itadani H, Nakamura T, Tanaka K, Ohta M;
 XX WPI; 2001-441675/47.
 XX DR N-PSDB; AAF47911.
 XX XX
 XX PT G protein-coupled receptor protein BG26, with activity of binding to
 XX PT histamine and capable of changing intracellular cAMP concentration in
 XX PT response to its stimulus, applicable as tool in screening ligands or drug
 XX PT candidates.
 XX PS
 XX PS Claim 1; Page 41-44; 50pp; Japanese.
 XX CC
 XX CC The present sequence is that of the human G protein-coupled receptor
 XX CC protein BG26, which shows significant homology with histamine H3, with
 XX CC activity of binding to histamine and capable of changing intracellular
 XX CC cAMP concentration in response to its stimulus. The protein is applicable
 XX CC as a tool in screening ligands or drug candidates for regulating signal
 XX CC transduction from such protein and treating diseases associated with its
 XX CC abnormality
 XX XX
 XX SQ Sequence 390 AA;
 Query Match 5.4%; Score 21; DB 4; Length 390;
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 TDYLLCTASVYNIVLISYDRY 113
 DB 93 TDYLLCTASVYNIVLISYDRY 113
 RESULT 11
 AAMS1410
 ID AAMS1410 standard; protein; 390 AA.
 XX AC AAMS1410;
 XX XX
 XX DT 07-JAN-2002 (first entry)
 XX XX
 XX DE Human GPRV53.
 XX KW Human; guanosine triphosphate-binding protein-coupled receptor; GPRV53;
 XX KW intracellular calcium ion regulation; histamine receptor; leukocyte.
 XX OS Homo sapiens.
 XX XX
 XX PN WO200173023-A1.
 XX PD 04-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-JP002767.
 XX XX
 XX PR 31-MAR-2000; 2000JP-00101339.
 XX PR 29-MAY-2000; 2000JP-00163147.
 XX PR 19-JUL-2000; 2000JP-00223870.
 XX XX
 XX PA (HELI-) HELIX RES INST.
 XX XX
 XX PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
 XX PI Sugiyama T;
 XX XX
 XX DR WPI; 2001-626265/72.
 XX DR N-PSDB; AAI66009.
 XX XX

XX PN EF1096009-A1.
 XX XX
 XX PD 02-MAY-2001.
 XX XX
 XX PF 24-OCT-2000; 2000EP-00309364.
 XX XX
 XX PR 29-OCT-1999; 99GB-00025641.
 XX PR 20-APR-2000; 2000GB-00009973.
 XX XX
 XX PA (PFI) PFIZER LTD.
 XX PA (PFI) PFIZER INC.
 XX XX
 XX PI Peter B, O'reilly MA;
 XX XX
 XX DR WPI; 2001-309854/33.
 XX DR N-PSDB; AAF83203.
 XX XX
 XX PT New G-protein coupled receptor-like polypeptide, polynucleotide for
 XX PT screening drug candidates for treating diseases associated with signal
 XX PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
 XX PS
 XX PS Claim 22; Page 44; 66pp; English.
 XX CC
 XX CC This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
 XX CC 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed
 XX CC by standard recombinant methodology. Antibodies and modulators of PFI-013
 XX CC are useful in the manufacture of a medicament for treating allergic
 XX CC disorder, including extrinsic asthma, immunological disorders, such as
 XX CC intrinsic asthma, vasculitic granulomatous disease, interstitial and
 XX CC other pulmonary disease, including chronic obstructive pulmonary disease
 XX CC (COPD), infectious, inflammatory disease, such as inflammatory bowel
 XX CC disease and neoplastic and myeloproliferative diseases. They are also
 XX CC useful for treating obesity, diabetes, reproductive and sexual medicine,
 XX CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,
 XX CC inflammation, cancer, tissue repair, dermatology, photoaging, skin
 XX CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,
 XX CC allergy and respiratory disease, sensory organ disorders, sleep disorders
 XX CC and hair loss. The PFI-013 protein and nucleic acid are useful in the
 XX CC diagnosis and treatment of the above conditions and also for screening
 XX CC drug candidates for the treatment of diseases associated with signal
 XX CC transduction. The antibodies are also useful for enrichment of
 XX CC eosinophils from mammalian, especially human blood and for detecting the
 XX CC protein in biological samples
 XX XX
 XX SQ Sequence 390 AA;
 Query Match 5.4%; Score 21; DB 4; Length 390;
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 TDYLLCTASVYNIVLISYDRY 113
 DB 93 TDYLLCTASVYNIVLISYDRY 113
 RESULT 10
 AAG64477
 ID AAG64477 standard; protein; 390 AA.
 XX AC AAG64477;
 XX XX
 XX DT 25-SEP-2001 (first entry)
 XX XX
 XX DE Human G protein-coupled receptor protein BG26.
 XX KW Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
 XX KW altering intracellular cAMP concentration;
 XX KW regulating signal transduction.
 XX OS Homo sapiens.
 XX XX
 XX PN WO200146414-A1.

PT Gene encoding a G-protein coupled histamine receptor protein for
PT identification of agonists and antagonists as drugs active in histamine-
XX related disorders.
XX
PS Claim 1; Page 42-43; 5lpp; Japanese.
XX
XX The invention relates to human G-protein coupled histamine receptor
CC GPRV53. GPRV53 is a new type of histamine receptor which is
CC preferentially expressed in peripheral leukocytes and on stimulation with
CC histamine causes a change in intracellular calcium ion concentration.
CC GPRV53 is useful in the identification of antagonists and agonists of
CC histamine binding to GPRV53 which can be used for the treatment and
CC prevention of histamine-associated disorders. Also, since the receptor
CC protein is preferentially expressed in tissues (especially in peripheral
CC leukocytes) other than those associated with the known histamine receptor
CC types H1-H3 it is useful in the investigation of the role of histamine
CC and its receptors in the tissues in which it is expressed
XX
SQ Sequence 390 AA;
Query Match 5.4%; Score 21; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 TDYLLCTASVYNNIVLISYDRY 113
DB |||||
93 TDYLLCTASVYNNIVLISYDRY 113
RESULT 12
ID AAB73622
XX AAB73622;
AC AAB73622;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human G protein-coupled receptor AXOR35.
XX
XX AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; bipolar disorder; depression; delirium; dementia;
KW severe mental retardation; dyskinesia; Parkinson's disease;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery.
XX
OS Homo sapiens.
XX
XX WO200133221-A1.
XX
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergema DJ, Fitzgerald LR, Graybill TL, Li X,
XX Michalovich D, Morrow DM, Zhu Y;
XX
XX WPI: 2001-316464/33.
XX
XX N-PSDB; AAB24007.

PT Novel G-protein coupled receptor polypeptide and polynucleotide for
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
PT disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 1; Page 50-51; 54pp; English.
XX
XX The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
CC and nucleotides may be used to treat a wide variety of disorders
CC including bacterial, fungal, protozoal and viral infections, particularly
CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
CC urinary retention; acute heart failure; hypotension; hypertension; angina
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia, and severe mental
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
CC antibodies may be used in screening compounds for their ability to
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
CC particularly useful for treating asthma, and inhibiting or promoting the
CC function of lymphocytes, macrophages, eosinophils or neutrophils in
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
CC useful for diagnosing or determining susceptibility of an individual to a
CC disease via the detection of abnormal levels of protein or mRNA, or via
CC the detection of mutations in the corresponding gene. AXOR35 proteins are
CC also useful for inducing an immunological response in a mammal against
CC the above diseases, and for antibody production. AXOR35 nucleotides are
CC also useful as diagnostic reagents, in chromosome localisation and tissue
CC expression studies, and for producing transgenic animals useful in drug
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
CC protein or fragments thereof, and are also useful for treating conditions
CC associated with the expression of the AXOR35 protein. The present
CC sequence represents human AXOR35
XX
SQ Sequence 390 AA;
Query Match 5.4%; Score 21; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 TDYLLCTASVYNNIVLISYDRY 113
DB |||||
93 TDYLLCTASVYNNIVLISYDRY 113
RESULT 13
AAM53050
ID AAM53050 standard; protein; 390 AA.
XX
XX AAM53050;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human G protein-coupled receptor NGPCR-2067.
XX
XX Human; NGPCR-2067; G protein-coupled receptor; 7TM receptor;
KW signal transduction; mental disorder; central nervous system disease;
KW metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
KW psychotic disorder; Huntington's disease; schizophrenia; migraine;
KW depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
KW Parkinson's disease; proliferative disorder; cancer; psoriasis;
KW benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;
KW thyroid disorder; cardiovascular disease; hypotension; hypertension;
KW thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
KW inflammatory conditions; autoimmune disorder; rheumatoid arthritis;

KW hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
KW anti-diabetic; metabolic; hypertensive; hypotensive; thrombolytic;
KW cardiatic; antiatherosclerotic; neuroleptic; anti-migraine;
KW antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
KW anticonvulsant; anti-inflammatory; antirheumatic; antiarthritic;
KW antipsoriatic; gene therapy; receptor.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 19..41
FT FT /label= Transmembrane_domain_1
FT Domain 52..74
FT FT /label= Transmembrane_domain_2
FT Domain 86..110
FT FT /label= Transmembrane_domain_3
FT Domain 128..146
FT FT /label= Transmembrane_domain_4
FT Domain 172..194
FT FT /label= Transmembrane_domain_5
FT Domain 305..326
FT FT /label= Transmembrane_domain_6
FT Domain 342..360
FT FT /label= Transmembrane_domain_7
XX
XX WO200185793-A2.
XX
XX 15-NOV-2001.
XX
XX 08-MAY-2001; 2001WO-US014750.
XX
XX 08-MAY-2000; 2000US-0203108P.
XX
XX (PTAA) PHARMACIA & UPJOHN CO.
XX
XX Lind P, Sejlitz T, Vogeli G, Wood LS;
XX
XX WPI; 2002-062240/08.
XX
XX N-PSDB; ABA02496.
XX
XX New polynucleotide, useful for identifying modulator compounds which are
XX used for treating psoriasis, schizophrenia, diabetes, encodes the novel G
XX protein-coupled receptor (ngPCR) polypeptide (ngPCR-2067).
XX
XX Claim 31; Page 63; 100pp; English.
XX
XX This sequence represents a novel human G protein-coupled receptor (GPCR)
XX designated ngPCR-2067. Like all GPCRs, ngPCR-2067 has 7 putative
XX transmembrane domains and is involved in signal transduction. The
XX invention also relates to expression vectors and host cells comprising
XX nucleic acids encoding ngPCR-2067, to recombinant expression of ngPCR-
XX 2067, to antibodies specific for ngPCR-2067, to drug screening methods
XX that use ngPCR-2067, and to modulators of ngPCR-2067 activity. ngPCR-2067
XX nucleic acid sequences may be used to isolate ngPCR-2067 allelic variants
XX and species homologues and may also be used in genetic mapping. The
XX invention also discloses the use of ngPCR-2067 nucleic acids in screening
XX for a predisposition to ngPCR-2067-associated hereditary mental
XX disorders, or for the diagnosis of these disorders. ngPCR-2067 nucleic
XX acids may additionally be used to generate transgenic animals, including
XX knockout animals, which may provide an insight into treating a variety of
XX human disorders, and may also be used in the design of antisense
XX molecules for suppressing expression of ngPCR-2067 in cells. ngPCR-2067,
XX and ngPCR-2067 modulators may be used to treat a wide variety of medical
XX conditions, particularly mental disorders, central nervous system
XX diseases, and metabolic diseases. Diseases that may be treated include
XX viral infections, particularly HIV-1 or HIV-2 infections; pain; central
XX nervous system, neurological and psychotic disorders such as Huntington's
XX disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,
XX dementia, Alzheimer's disease, and Parkinson's disease; proliferative
XX disorders such as cancers, benign prostatic hypertrophy and psoriasis;
XX metabolic disorders such as diabetes, dyslipidaemia, obesity, and
XX anorexia; thyroid disorders; cardiovascular diseases such as hypotension,
XX hypertension, thrombosis, myocardial infarction, cardiomyopathies, and

CC atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
CC rheumatoid arthritis); hormonal disorders; and renal failure
XX
XX Sequence 390 AA;
XX
XX Query Match 5.4%; Score 21; DB 5; Length 390;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-12;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 93 TDYLLCTASVNVNVLISYDRY 113
XX |||||
XX 93 TDYLLCTASVNVNVLISYDRY 113
XX |||||
XX
XX RESULT 14
XX ABP98629
XX ID ABP98629 standard; protein; 390 AA.
XX
XX AC ABP98629;
XX
XX DT 13-JUN-2003 (first entry)
XX
XX DE Human histamine receptor SP9144.
XX
XX KW human; histamine receptor; chromosome 18; anti-inflammatory;
XX KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
XX KW anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;
XX KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
XX KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
XX KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
XX KW psoriasis; receptor.
XX
XX OS Homo sapiens.
XX
XX PN US6204017-B1.
XX
XX PD 20-MAR-2001.
XX
XX PF 07-OCT-1999; 99US-00414010.
XX
XX PR 07-OCT-1999; 99US-00414010.
XX
XX PA (SCHE) SCHERING CORP.
XX
XX PI Behan JX, Hedrick JA, Laz TW, Monsma FJ, Morse KL, Umland SP;
XX PI Wang S,
XX
XX WPI; 2002-442063/47.
XX N-PSDB; ABZ80663.
XX
XX New nucleic acid encoding antigenic part of human histamine receptor,
XX useful for preparing antibodies, e.g. for treating-histamine related
XX disorders.
XX
XX Example 1; Col 27-30; 19pp; English.
XX
XX This sequence represents the amino acid sequence of a human histamine
XX receptor (HR) designated SP9144. The sequence was isolated by searching
XX databases with the sequence of known G-coupled protein receptor (GPCR).
XX The gene is used for recombinant production of HR and for preparing
XX antibodies (Ab). These Ab are used to purify HR by immunoaffinity
XX chromatography, in immunoassay of histamine receptor, to identify cDNA
XX clones that express the receptor, as antagonist to block binding of
XX histamine (for treating any histamine-associated disorder) and to
XX generate anti-idiotypic antibodies. Agonists and antagonists of the HR
XX protein can be used in the treatment of e.g. inflammation, asthma,
XX allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
XX chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
XX sclerosis, inflammatory bowel disease and psoriasis
XX
XX Sequence 390 AA;
XX
XX Query Match 5.4%; Score 21; DB 5; Length 390;

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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:24:15 ; Search time 32 Seconds
(without alignments)
630.805 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSSESTGILPPAAQVPLAF.....WKILCVTKWPAISQNSQSVSS 391

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
 - 3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep:*
 - 4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep:*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	5.4	390	3	US-09-414-010-2
2	21	5.4	390	4	US-09-812-216-2
3	11	2.8	19	2	US-08-985-090-8
4	11	2.8	19	3	US-09-165-543-8
5	11	2.8	19	3	US-09-165-543-15
6	11	2.8	351	4	US-09-524-162-2
7	11	2.8	445	2	US-08-985-090-2
8	11	2.8	445	3	US-09-165-543-2
9	11	2.8	445	3	US-09-165-543-5
10	11	2.8	445	3	US-09-167-354-7
11	11	2.8	445	4	US-09-642-855-7
12	11	2.8	445	4	US-09-642-514-7
13	9	2.3	362	2	US-08-985-090-5
14	9	2.3	362	3	US-09-165-543-32
15	9	2.3	384	2	US-08-833-226-2
16	8	2.0	252	4	US-09-107-532A-4457
17	7	1.8	22	2	US-08-985-090-9
18	7	1.8	22	2	US-08-985-090-15
19	7	1.8	22	3	US-09-165-543-9
20	7	1.8	22	3	US-09-165-543-16
21	7	1.8	22	3	US-09-165-543-35
22	7	1.8	34	3	US-09-177-249-243
23	7	1.8	57	4	US-09-621-976-5298
24	7	1.8	87	3	US-09-087-232A-18
25	7	1.8	96	4	US-09-489-039A-14289
26	7	1.8	100	3	US-09-087-232A-15
27	7	1.8	110	1	US-08-466-886-32

28	7	1.8	110	3	US-08-469-617-32	Sequence 32, Appl
29	7	1.8	122	4	US-09-489-039A-8669	Sequence 8669, Ap
30	7	1.8	146	4	US-09-252-991A-31678	Sequence 31678, A
31	7	1.8	153	2	US-08-896-365-9	Sequence 9, Appli
32	7	1.8	184	4	US-08-833-752-4	Sequence 4, Appli
33	7	1.8	194	4	US-09-489-039A-9376	Sequence 9376, Ap
34	7	1.8	212	2	US-08-753-159A-4	Sequence 4, Appli
35	7	1.8	212	3	US-09-133-735-4	Sequence 4, Appli
36	7	1.8	215	3	US-09-087-232A-17	Sequence 17, Appl
37	7	1.8	215	4	US-08-833-752-6	Sequence 6, Appli
38	7	1.8	224	4	US-09-489-039A-8543	Sequence 8543, Ap
39	7	1.8	233	4	US-09-252-991A-27758	Sequence 27758, A
40	7	1.8	257	2	US-08-896-365-8	Sequence 8, Appli
41	7	1.8	260	4	US-09-252-991A-31019	Sequence 31019, A
42	7	1.8	263	4	US-09-252-991A-30502	Sequence 30502, A
43	7	1.8	288	2	US-08-466-103A-6	Sequence 6, Appli
44	7	1.8	329	4	US-09-502-783A-9	Sequence 9, Appli
45	7	1.8	342	1	US-08-244-646-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2

Query Match 5.4%; Score 21; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVNVIVLSYDRY 113
DB 93 TDYLLCTASVNVIVLSYDRY 113

RESULT 2
US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010

;; PRIOR FILING DATE: 1999-10-07
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 390
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 5.4%; Score 21; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYINVLISYDRY 113
Db 93 TDYLLCTASVYINVLISYDRY 113

RESULT 3

US-08-985-090-8
; Sequence 8, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/08/985,090
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jean M. Silveri
;; REGISTRATION NUMBER: 39,030
;; REFERENCE/DOCKET NUMBER: MNI-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-985-090-8

Query Match 2.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LNLAISDFLVG 65
Db 2 LNLAISDFLVG 12

RESULT 4

US-09-165-543-8
; Sequence 8, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:

;; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
;; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
;; NUMBER OF SEQUENCES: 39
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/09/165,543
;; FILING DATE:
;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/042,780
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elizabeth A. Hanley
;; REGISTRATION NUMBER: 33,505
;; REFERENCE/DOCKET NUMBER: MNI-032CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
US-09-165-543-8

Query Match 2.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LNLAISDFLVG 65
Db 2 LNLAISDFLVG 12

RESULT 5

US-09-165-543-15
; Sequence 15, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/09/165,543
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/042,780

ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-165-543-15

Query Match 2.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAIISDFLVG 65
Db 2 LNLAIISDFLVG 12

RESULT 6
US-09-524-162-2
Sequence 2, Application US/09524162
Patent No. 6355452
GENERAL INFORMATION:
APPLICANT: Ping Tsui
TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
FILE REFERENCE: GP-70681
CURRENT APPLICATION NUMBER: US/09/524,162
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 351
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-524-162-2

Query Match 2.8%; Score 11; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAIISDFLVG 65
Db 74 LNLAIISDFLVG 84

RESULT 7
US-08-985-090-2
Sequence 2, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-090-2

Query Match 2.8%; Score 11; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAIISDFLVG 65
Db 74 LNLAIISDFLVG 84

RESULT 8
US-09-165-543-2
Sequence 2, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-165-543-2

Query Match 2.8%; Score 11; DB 3; Length 445;

Best Local Similarity 100.0%; Pred. No. 0.045; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65
Db 74 LNLAISDFLVG 84

RESULT 9

US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MMI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-5

Query Match 2.8%; Score 11; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65
Db 74 LNLAISDFLVG 84

RESULT 10

US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-167-354-7

Query Match 2.8%; Score 11; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65
Db 74 LNLAISDFLVG 84

RESULT 11

US-09-642-855-7
; Sequence 7, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-855-7

Query Match 2.8%; Score 11; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65
Db 74 LNLAISDFLVG 84

RESULT 12

US-09-642-514-7
; Sequence 7, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7

; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-514-7

Query Match 2.8%; Score 11; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.045; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65
DB 74 LNLAISDFLVG 84

RESULT 13
US-08-985-090-5
; Sequence 5, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-5

Query Match 2.3%; Score 9; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 NIVLISYDR 112
DB 41 NIVLISYDR 49

RESULT 14
US-09-165-543-32
; Sequence 32, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-32

Query Match 2.3%; Score 9; DB 3; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 NIVLISYDR 112
DB 41 NIVLISYDR 49

RESULT 15
US-08-833-226-2
; Sequence 2, Application US/08833226
; Patent No. 5891720
; GENERAL INFORMATION:
; APPLICANT: Moore, Karen
; APPLICANT: Nagle, Deborah
; APPLICANT: Woolf, Elizabeth
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,226
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-833-226-2

Query Match 2.3% Score 9; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64
|||
Db 94 NLAISDFLV 102
|||
|||

Search completed: October 1, 2004, 10:30:22
Job time : 33 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:29:06 ; Search time 134 Seconds
(without alignments)
938.981 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSESSTGILPPAAQVPLAF.....WKILCTKWPALSONQSVSS 391

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA.*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	5.4	73	10 US-09-782-974C-6	Sequence 6, Appli
2	21	5.4	390	9 US-09-910-411-2	Sequence 2, Appli
3	21	5.4	390	10 US-09-852-165-2	Sequence 2, Appli
4	21	5.4	390	10 US-09-891-138A-6	Sequence 6, Appli
5	21	5.4	390	12 US-10-349-253A-2	Sequence 2, Appli
6	21	5.4	390	12 US-09-875-076-14	Sequence 14, Appl
7	21	5.4	390	12 US-09-876-252-14	Sequence 14, Appl
8	21	5.4	390	13 US-10-052-193-2	Sequence 14, Appl
9	21	5.4	390	14 US-10-225-567A-629	Sequence 27, Appl
10	21	5.4	390	14 US-10-290-078-27	Sequence 27, Appl
11	21	5.4	390	14 US-10-272-981-14	Sequence 14, Appl
12	21	5.4	390	14 US-10-354-769-2	Sequence 14, Appl
13	21	5.4	390	14 US-10-393-807-14	Sequence 14, Appl
14	21	5.4	390	15 US-10-417-820A-14	Sequence 14, Appl
15	21	5.4	390	16 US-10-696-673-2	Sequence 2, Appli

16	21	5.4	390	16	US-10-723-955-14	Sequence 14, Appl
17	21	5.4	390	16	US-10-737-619-2	Sequence 2, Appli
18	21	5.4	390	16	US-10-782-596-14	Sequence 14, Appl
19	21	5.4	441	16	US-10-398-036-3	Sequence 3, Appli
20	11	2.8	19	9	US-09-350-206-8	Sequence 8, Appli
21	11	2.8	19	9	US-09-350-206-15	Sequence 15, Appl
22	11	2.8	19	9	US-09-349-755-8	Sequence 8, Appli
23	11	2.8	19	9	US-09-349-755-15	Sequence 8, Appli
24	11	2.8	19	9	US-09-166-334-8	Sequence 15, Appl
25	11	2.8	19	9	US-09-166-334-15	Sequence 8, Appli
26	11	2.8	19	14	US-10-282-958-15	Sequence 15, Appl
27	11	2.8	19	14	US-10-282-958-15	Sequence 15, Appl
28	11	2.8	168	10	US-09-791-279-147	Sequence 147, Appl
29	11	2.8	413	12	US-09-891-053-1	Sequence 1, Appli
30	11	2.8	445	9	US-09-350-206-2	Sequence 2, Appli
31	11	2.8	445	9	US-09-350-206-5	Sequence 5, Appli
32	11	2.8	445	9	US-09-349-755-2	Sequence 2, Appli
33	11	2.8	445	9	US-09-349-755-5	Sequence 5, Appli
34	11	2.8	445	9	US-09-166-334-2	Sequence 2, Appli
35	11	2.8	445	9	US-09-166-334-5	Sequence 5, Appli
36	11	2.8	445	12	US-09-891-053-25	Sequence 25, Appl
37	11	2.8	445	14	US-10-282-958-2	Sequence 2, Appli
38	11	2.8	445	14	US-10-282-958-5	Sequence 5, Appli
39	11	2.8	445	14	US-10-225-567A-549	Sequence 549, App
40	11	2.8	445	16	US-10-453-106-1	Sequence 2, Appli
41	11	2.8	445	16	US-10-453-106-2	Sequence 2, Appli
42	11	2.8	445	16	US-10-453-106-3	Sequence 3, Appli
43	11	2.8	445	16	US-10-727-021-7	Sequence 7, Appli
44	11	2.8	453	12	US-09-891-053-20	Sequence 20, Appl
45	9	2.3	22	14	US-10-067-649-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-782-974C-6
; Sequence 6, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 73

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-6

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Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIVLISYDRY 113
Db 31 TDYLLCTASVYNIVLISYDRY 51

RESULT 2
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-411-2

Query Match      5.4%; Score 21; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIVLISYDRY 113
Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 3
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231resus
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

Query Match      5.4%; Score 21; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIVLISYDRY 113
Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 4
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1 Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match      5.4%; Score 21; DB 10; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIVLISYDRY 113
Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 5
US-10-349-253A-2
; Sequence 2, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-349-253A-2

Query Match 5.4%; Score 21; DB 12; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113
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Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 6

US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 5.4%; Score 21; DB 12; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113
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Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 7

US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match 5.4%; Score 21; DB 12; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIIVLSYDRY 113
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Db 93 TDYLLCTASVYNIIVLSYDRY 113

RESULT 8
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

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Db 93 TDYLLCTASVYNIIVLSYDRY 113

RESULT 9
US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match 5.4%; Score 21; DB 14; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIIVLSYDRY 113
|||
Db 93 TDYLLCTASVYNIIVLSYDRY 113

RESULT 10
US-10-290-078-27
; Sequence 27, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692 or 58874
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-078-27

Query Match 5.4%; Score 21; DB 14; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIIVLSYDRY 113
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Db 93 TDYLLCTASVYNIIVLSYDRY 113

RESULT 11
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12

APPLICANT: Liaw, Chen W.

PRIOR FILING DATE: 1

APPLICANT: Liaw, Chen W.

Mon Oct 4 10:27:26 2004

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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-14
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Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 93 TDYLLCTASVYNIVLISYDRY 113
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RESULT 15
US-10-696-673-2
; Sequence 2, Application US/10696673
; Publication No. US20040105846A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: PHRM0025-101/00231REGUS.1 DVI
; CURRENT APPLICATION NUMBER: US/10/696,673
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/203,108
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/852,165
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-696-673-2
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Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 93 TDYLLCTASVYNIVLISYDRY 113
Db 93 TDYLLCTASVYNIVLISYDRY 113
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Search completed: October 1, 2004, 10:41:05
Job time : 135 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:23:00 ; Search time 41 Seconds
(without alignments)
917.339 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSESNSGTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

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Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78.*

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2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	8	2.0	368	A52450	cysteine synthase
5	8	2.0	400	S64729	protein secretion
6	8	2.0	426	H75578	phenylacetyl-CoA l
7	8	2.0	561	A44128	(N-acetylneuraminy
8	7	1.8	32	B38839	histone H1 - sea u
9	7	1.8	55	AE2381	type I site-specif
10	7	1.8	98	AG1960	hypothetical prote
11	7	1.8	103	H81841	hypothetical prote
12	7	1.8	108	H81098	hypothetical prote
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25	7	1.8	257	A96546	probable peptide m
26	7	1.8	271	B35407	unknown protein [i
27	7	1.8	280	D86870	tryptophan synthas
28	7	1.8	308	I50241	hypothetical prote
29	7	1.8	326	T04344	G protein-coupled p
					eroxidase (EC 1.1

30 7 1.8 334 2 H95342 NosX protein requi
31 7 1.8 342 2 S23764 polygalacturanase-
32 7 1.8 350 2 I38848 Mel-1a melatonin r
33 7 1.8 352 2 A43113 chemokine (C-C) re
34 7 1.8 354 2 C45229 opsin, rod ultravi
35 7 1.8 355 2 G02436 chemokine (C-C) re
36 7 1.8 355 2 C45229 chemokine (C-C) re
37 7 1.8 360 2 A51777 chemokine (C-C) re
38 7 1.8 360 2 A51760 chemokine (C-C) re
39 7 1.8 360 2 JC4587 chemokine (C-C) re
40 7 1.8 361 2 B86692 chemokine (C-C) re
41 7 1.8 362 2 I38990 chemokine (C-C) re
42 7 1.8 366 2 I46469 Mel-1a melatonin r
43 7 1.8 370 1 BVLVMX mbpX protein - liv
44 7 1.8 371 2 A39234 opsin - bluebottle
45 7 1.8 373 1 OOFF rhodopsin - fruit

ALIGNMENTS

RESULT 1
JC7566
histamine H4 receptor, HH4R - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C/Accession: JC7566
R/Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.
Biochem. Biophys. Res. Commun. 279, 615-620, 2000
A/Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.
A/Reference number: JC7566; MUID: 20568725; PMID:11118334
A/Contents: Leukocyte
A/Accession: JC7566
A/Molecule type: mRNA
A/Residues: 1-390 <NAK>
A/Cross-references: DDBJ:AB045370
C/Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled
C/Genetics:
A/Gene: hh4r
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.4%; Score 21; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIIVLSYDHY 113

DB 93 TDYLLCTASVYNIIVLSYDHY 113

RESULT 2
AE3523
icc protein [imported] - Brucella melitensis (strain 16M)
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 02-Aug-2002
C/Accession: AE3523
R/DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A/Reference number: AD3252; PMID:11756688
A/Accession: AE3523
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-281 <KUR>
A/Cross-references: GB:AE008918; PIDN:AAU53352.1; PID:gl7984241; GSPDB:GN00191
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BMEI0111
A/Map position: II
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase cpdA; 3',5'-cyclic-nucleotide p

Query Match 2.0%; Score 8; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 6.4; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 ASGHLHRA 232
DB 191 ASGHLHRA 198

RESULT 3
T22636
hypothetical protein F54C9.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22636
R:Sims, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19591
A:Accession: T22636
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-328 <WIL>
A:Cross-references: EMBL:Z49967; PIDN:CAA90256.1; GSPDB:GN00020; CESP:F54C9.11
A:Experimental source: clone F54C9
C:Genetics:
A:Gene: CESP:F54C9.11
A:Map position: 2
A:Introns: 24/2; 92/3

Query Match 2.0%; Score 8; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 STTSSAS 226
DB 29 STTSSAS 36
RESULT 4
A55450
cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach
C:Species: Spinacia oleracea (spinach)
C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 20-Jun-2000
C:Accession: A55450
R:Saico, K.; Tatsuguchi, K.; Takagi, Y.; Murakoshi, I.
J. Biol. Chem. 269, 28187-28192, 1994
A:Title: Isolation and characterization of cDNA that encodes a putative mitochondrial-located
A:Reference number: A55450; MUID:95050598; PMID:7961755
A:Accession: A55450
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-368 <SAI>
A:Cross-references: GB:D37963; NID:g1066152; PIDN:BAA07177.1; PID:g1066153
C:Superfamily: threonine dehydratase
C:Keywords: carbon-oxygen lyase; cysteine biosynthesis; mitochondrion; phosphoprotein; F;1-33/Domain: transit peptide (mitochondrion) #status predicted <PP>
F;34-368/Product: cysteine synthase C #status predicted <MAT>
F;90/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 2.0%; Score 8; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 8.2; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 FSTTSSA 225
DB 26 FSTTSSA 33
RESULT 5
S64729
protein secretion protein xcpS - Pseudomonas putida
C:Species: Pseudomonas putida
C>Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2000
C:Accession: S64729; S47506

R:de Groot, A.; Krijger, J.J.; Filloux, A.; Tommassen, J.
Mol. Gen. Genet. 250, 491-504, 1996
A:Title: Characterization of type II protein secretion (xcp) genes in the plant growth-stimulating bacterium *Agrobacterium tumefaciens* strain C58
A:Reference number: S64724; MUID:96186881; PMID:8602167
A:Accession: S64729
A:Molecule type: DNA
A:Residues: 1-400 <DEG>
A:Cross-references: EMBL:X81085; NID:g3293032; PIDN:CAA56981.1; PID:g531742
C:Genetics:
A:Gene: xcpS
C:Superfamily: secretion protein xcpS

Query Match 2.0%; Score 8; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 8.8; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 LARSALIL 310
DB 268 LARSALIL 275

RESULT 6
H75578
phenylacetyl-CoA ligase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: H75578
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, H.O.; Venter, J.C.; Fraser, C.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567286
A:Accession: H75578
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <WHI>
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12384.1; PID:g646067
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0256
A:Map position: 2
C:Superfamily: coenzyme F390 synthetase II

Query Match 2.0%; Score 8; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 SESALRQ 291
DB 377 SESALRQ 384

RESULT 7
A44128
(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (EC 2 C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2003
C:Accession: A44128
R:Nagata, Y.; Yamashiro, S.; Yodoi, J.; Lloyd, K.O.; Shiku, H.; Furukawa, K. J. Biol. Chem. 267, 12082-12089, 1992
A:Title: Expression cloning of beta 1,4 N-acetylgalactosaminyltransferase cDNAs that detect
A:Reference number: A44128; MUID:92291088; PMID:1601877
A:Accession: A44128
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-561 <NAG>
A:Experimental source: NK-like cell line YT
C:Superfamily: (N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 2.0%; Score 8; DB 1; Length 561;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 STSSAS 226
|||||
Db 419 STSSAS 426

RESULT 8
B38839
histone H1 - sea urchin (Strongylocentrotus intermedius) (fragment)
C;Species: Strongylocentrotus intermedius
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 12-Apr-1995
C;Accession: B38839
R;Suzuki, M.; Sugitara, M.; Ebashi, S.
J. Biochem. 108, 347-355, 1990
A;Title: Sea urchin protease specific to the SPKK motif in histone.
A;Reference number: P90145; MUID:91115778; PMID:2126010
A;Accession: B38839
A;Molecule type: Protein
A;Residues: 1-32 <SUZ>
C;Superfamily: histone H1
C;Keywords: chromosomal protein; nucleosome

Query Match 1.8%; Score 7; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 SPRKSS 260
|||||
Db 22 SPRKSS 28

RESULT 9
AE2381
type I site-specific deoxyribonuclease chain R [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2381
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2381
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-55 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA076304.1; PID:gl7133742; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr4605

Query Match 1.8%; Score 7; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 ALSQNS 388
|||||
Db 9 ALSQNS 15

RESULT 10
AG1960
hypothetical protein asr1234 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1960
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG1960
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA073191.1; PID:gl7130581; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr1234

Query Match 1.8%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 LTITML 183
|||||
Db 32 LTITML 38

RESULT 11

H81841
hypothetical protein NMA1503 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81841
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: H81841
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <PAR>
A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84735.1; PID:g7380150
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1503
C;Superfamily: Neisseria meningitidis hypothetical protein NMA1503

Query Match 1.8%; Score 7; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LAILLSA 313
|||||
Db 2 LAILLSA 8

RESULT 12

H81098
hypothetical protein NMB1293 [imported] - Neisseria meningitidis (strain MCS8 serogroup F
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: H81098
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81098
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <TET>
A;Cross-references: GB:AE002478; GB:AE002098; NID:g7226533; PIDN:AAF41669.1; PID:g7226534
A;Experimental source: serogroup B, strain MCS8
C;Genetics:
A;Gene: NMB1293
C;Superfamily: Neisseria meningitidis hypothetical protein NMA1503

Mon Oct 4 10:27:26 2004

us-10-626-445-8.olog.rpr

Query Match 1.8%; Score 7; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LAIILSA 313
|||||
Db 7 LAIILSA 13

RESULT 13

TI6798
hypothetical protein T04A6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16798
R;Vaudin, M.; Anderson, K.
submitted to the EMBL Data Library, April 1994
A;Description: The sequence of C. elegans cosmid T04A6.
A;Reference number: Z18579
A;Accession: T16798
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-111 <VAU>
A;Cross-references: EMBL:U00042; NID:g470332; PID:g470333; PIDN:AAA50672.1; CESP:T04A6.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T04A6.1
A;Introns: 11/3; 82/1

Query Match 1.8%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 LPVISVA 193
|||||
Db 25 LPVISVA 31

RESULT 14

I84498
melatonin receptor - striped hairy-footed hamster (fragment)
C;Species: Phodopus sungorus (striped hairy-footed hamster)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Apr-2000
C;Accession: I84498
R;Reppert, S.M.; Weaver, D.R.; Ebisawa, T.
Neuron 13, 1177-1185, 1994
A;Title: Cloning and characterization of a mammalian melatonin receptor that mediates re
A;Reference number: I38848; MUID:95033233; PMID:7946354
A;Accession: I84498
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-156 <RES>
A;Cross-references: EMBL:U14110; NID:g602133; PID:g602134
C;Superfamily: vertebrate rhodopsin

Query Match 1.8%; Score 7; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 FAICWAP 320
|||||
Db 121 FAICWAP 127

RESULT 15

A83307
conserved hypothetical protein PA2713 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83307
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <STO>
A;Cross-references: GB:AE004699; GB:AE004091; NID:g9948782; PIDN:AAG06101.1; GSPDB:GN001;
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2713

Query Match 1.8%; Score 7; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 ARSLAIL 310
|||||
Db 14 ARSLAIL 20

Search completed: October 1, 2004, 10:29:45
Job time : 43 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:13:35 ; Search time 25 Seconds
(without alignments)
814.377 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 391
Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	5.4	390	1 HH4R HUMAN	Q9h3n8 homo sapien
2	11	2.8	445	1 HH3R CAVPO	Q9j135 cavia porce
3	11	2.8	445	1 HH3R HUMAN	Q9y5n1 homo sapien
4	11	2.8	445	1 HH3R MOUSE	P58406 mus musculus
5	11	2.8	445	1 HH3R RAT	Q9gyn8 rattus norv
6	9	2.3	309	1 CLT2 RAT	Q924t9 rattus norv
7	9	2.3	381	1 PKR2 MOUSE	Q8k458 mus musculus
8	9	2.3	383	1 PKR2 RAT	Q8r415 rattus norv
9	9	2.3	384	1 PKR2 BOVIN	Q8spn1 bos taurus
10	9	2.3	384	1 PKR2 HUMAN	Q8n1j6 homo sapien
11	9	2.3	393	1 PKR1 BOVIN	Q8spn2 bos taurus
12	9	2.3	393	1 PKR1 HUMAN	Q8tcw9 homo sapien
13	9	2.3	393	1 PKR1 MOUSE	Q9jkl1 mus musculus
14	9	2.3	393	1 PKR1 RAT	Q8r416 rattus norv
15	8	2.0	378	1 OPSD CAMAB	Q17292 camponotus
16	8	2.0	378	1 OPSD CARBO	Q17296 cataglyphis
17	8	2.0	640	1 PLB XLULA	Q59863 kluyveromyc
18	7	1.8	153	1 ML13 BRARE	P51049 brachydanio
19	7	1.8	154	1 ML1A PIG	O02781 sus scrofa
20	7	1.8	173	1 CLF8 MOUSE	Q8czr4 mus musculus
21	7	1.8	202	1 RNFG BUCAP	Q8kai8 buchera ap
22	7	1.8	212	1 ER21 BOVIN	P33946 bos taurus
23	7	1.8	212	1 ER21 HUMAN	P24390 homo sapien
24	7	1.8	257	1 ML1A BOVIN	O02769 bos taurus
25	7	1.8	271	1 TRPA THETH	P16608 thermus the
26	7	1.8	308	1 P2Y5 CHICK	P32250 gallus gall
27	7	1.8	342	1 PG11 PHAVU	P35334 phaseolus v
28	7	1.8	342	1 PG13 PHAVU	P58823 phaseolus v
29	7	1.8	345	1 CLT2 PIG	Q95n03 sus scrofa
30	7	1.8	346	1 CLT2 HUMAN	Q9ns75 homo sapien
31	7	1.8	350	1 ML1A HUMAN	P48039 homo sapien
32	7	1.8	352	1 CKR5 CERAE	P56493 cercopithec
33	7	1.8	352	1 CKR5 CERPY	Q9tv42 cercopithec

RESULT 1

ID	HH4R HUMAN	STANDARD;	PRT;	390 AA.
AC	Q9H3N8; Q9GZQ0;			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)			
DE	(GPCR105) (SP9144) (AXORJ5).			
GN	HRH4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]_TaxID:9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20538417; PubMed=10973974;			
RA	Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.-I.;			
RT	"Molecular cloning and characterization of novel type of histamine			
RT	receptor preferentially expressed in leukocytes.";			
RL	J. Biol. Chem. 275:36781-36786(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RX	TISSUE=Leukocyte;			
RC	MEDLINE=20568725; PubMed=11118334;			
RA	Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;			
RT	"Molecular cloning and characterization of a new human histamine			
RT	receptor, HH4R.";			
RL	Biochem. Biophys. Res. Commun. 279:615-620(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Jones P.G., Wu S., Betty M.;			
RT	"Cloning of a novel histamine receptor.";			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Bone marrow;			
RX	PubMed=11179434;			
RA	Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,			
RA	Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;			
RT	"Cloning and pharmacological characterization of a fourth histamine			
RT	receptor (H4) expressed in bone marrow.";			
RL	Mol. Pharmacol. 59:420-426(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Eosinophil;			
RX	MEDLINE=21104636; PubMed=11181941;			
RA	Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,			
RA	Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,			
RA	Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,			
RA	Monsma F.J. Jr.;			
RT	"Cloning and characterization of a novel human histamine receptor.";			
RL	J. Pharmacol. Exp. Ther. 296:1058-1066(2001).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21106320; PubMed=11179436;			

Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,
 Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,
 Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
 Bergsma D.J., Fitzgerald L.R.; and pharmacological characterization of a novel
 human histamine receptor.
 Mol. Pharmacol. 59:434-441 (2001).
 [7]
 SEQUENCE FROM N.A.
 RA O'Reilly M.A.;
 RT "Identification of a histamine H4 receptor on human eosinophils - Role
 in eosinophil chemotaxis.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 [8]
 SEQUENCE FROM N.A.
 RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: The H4 subclass of histamine receptors could mediate the
 histamine signals in peripheral tissues. Displays a significant
 level of constitutive activity (spontaneous activity in the
 absence of agonist).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and
 eosinophils. Shows preferential distribution in cells of
 immunological relevance such as T-cells, dendritic cells,
 monocytes, mast cells, neutrophils. Also expressed in a wide
 variety of peripheral tissues, including the heart, kidney, liver,
 lung, pancreas, skeletal muscle, prostate, small intestine,
 spleen, fetal liver and lymph node.
 CC -!- INDUCTION: Expression is either up-regulated or down-regulated
 upon activation of the lymphoid tissues and this regulation may
 depend on the presence of IL-10 or IL-13.
 CC -!- MISCELLANEOUS: Does not bind diphenhydramine, lorazepam,
 ranitidine, cimetidine and chlorpheniramine. Shows modest affinity
 for dimaprit, imipramine, clobenpropit, thioeramide, burimamide
 clozapine, imipip and imetit. The order of inhibitory activity
 was imetit > clobenpropit > burimamide > thioeramide.
 CC Clobenpropit behaves as a partial agonist, dimaprit and
 imipramine show some agonist activity while clozapine behaves as
 a full agonist. Thioeramide shows inverse agonism (enhances CAMP
 activity). The order of inhibitory activity of histamine
 derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-
 methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-
 methylhistamine > R(-)-alpha-methylhistamine behave as full
 agonists.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 or send an email to license@isb-sib.ch).

 CC EMBL; AB044934; BAB13698.1; -
 CC EMBL; AB045370; BAB20091.1; -
 CC EMBL; AF307973; AAG32052.1; -
 CC EMBL; AF312230; AAK12081.1; -
 CC EMBL; AF329449; AAK43542.1; -
 CC EMBL; AF325356; AAL01684.1; -
 CC EMBL; AJ298292; CAC83493.1; -
 CC EMBL; AJ136745; AAN01271.1; -
 CC PIR; JC7566; JC7566.
 CC Genew; HGNC:17383; HRH4.
 CC MIM; 606792; -
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0004969; F:histamine receptor activity; NAS.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC InterPro; IPR008102; Histamine_H4.
 CC Pfam; PF00001; 7tm_1; 1.

 RA PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01726; HISTAMINEH4R.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Lipoprotein; Palmitate.
 FT DOMAIN 1 19
 FT TRANSMEM 20 40
 FT DOMAIN 41 52
 FT TRANSMEM 53 73
 FT DOMAIN 74 87
 FT TRANSMEM 88 108
 FT DOMAIN 109 131
 FT TRANSMEM 132 152
 FT DOMAIN 153 172
 FT TRANSMEM 173 193
 FT DOMAIN 194 304
 FT TRANSMEM 305 325
 FT DOMAIN 326 341
 FT TRANSMEM 342 362
 FT DOMAIN 363 390
 FT DISULFID 87 164
 FT CARBOHYD 5 9
 FT CARBOHYD 374 374
 FT LIPID 138 138
 FT CONFLICT 206 206
 FT CONFLICT 253 253
 FT CONFLICT 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;
 SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;
 Query Match 5.48; Score 21; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 2e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 TDYLLCTASVNVNVLISYDRY 113
 DB 93 TDYLLCTASVNVNVLISYDRY 113
 RESULT 2
 HH3R_CAVPO STANDARD; PRT; 445 AA.
 ID HH3R_CAVPO STANDARD; PRT; 445 AA.
 AC Q9UJ35; Q9UJ36;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Histamine H3 receptor (HH3R).
 GN HRH3.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1] SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RP TISSUE=Brain;
 RC MEDLINE=2018440; PubMed=10757514;
 RA Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,
 Cochois V., Schwartz J.-C., Arrang J.-M.;
 RT "Cloning and cerebral expression of the guinea pig histamine H3
 receptor: evidence for two isoforms.";
 RL NeuroReport 11:755-759 (2000).
 CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
 histamine signals in CNS and peripheral nervous system. Signals
 through the inhibition of adenylyate cyclase and displays high
 constitutive activity (spontaneous activity in the absence of
 agonist).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long; Synonyms=H3L;
 CC IsoId=Q9UJ35-1; Sequence=Displayed;
 CC Name=Short; Synonyms=H3S;
 CC IsoId=Q9UJ35-2; Sequence=VSP_001880;

CC -!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the
 CC brain. Highly expressed in discrete neuronal populations such as
 CC pyramidal cells in cerebral cortex or cerebellar purkinje cells.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF267537; AAF78947.1; -;
 CC EMBL: AF267538; AAF78950.1; -;
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC DR InterPro; IPR003980; H3_receptor.
 CC DR Pfam; PF00001; 7tm 1; 1.
 CC DR PRINTS; PR00237; GPCRHOPOPSN.
 CC DR PRINTS; PR01471; HISTAMINEH3R.
 CC DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 CC DR PROSITE; PS00262; G PROTEIN RECP F1.2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Alternative splicing.
 FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 41 61 POTENTIAL.
 FT DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 72 92 POTENTIAL.
 FT DOMAIN 93 109 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 110 130 POTENTIAL.
 FT DOMAIN 131 157 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 158 178 POTENTIAL.
 FT DOMAIN 179 197 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 198 218 POTENTIAL.
 FT DOMAIN 219 359 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 360 380 POTENTIAL.
 FT DOMAIN 381 398 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 399 419 POTENTIAL.
 FT DOMAIN 420 445 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 20 24 POLY-ALA.
 FT DOMBOHD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 276 305 Missing (in isoform Short).
 FT SQ SEQUENCE 445 AA; 48734 MW; BAE206A3887189A0 CRC64;
 Query Match 2.8%; Score 11; DB 1; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 55 LNLAISDFLVG 65
 Db 75 LNLAISDFLVG 85
 |||||
 [1]
 RESULT 3
 ID H3R HUMAN STANDARD; PRT; 445 AA.
 AC Q9Y5N1; Q9GXZ2; Q9H4K3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
 OS HH3R OR GPCR97.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thalamus;
 RX MEDLINE=99278519; PubMed=10347254;
 RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
 RA Huvar A., Jackson M.R., Belzander M.G.,

RT "Cloning and functional expression of the human histamine H3
 RL receptor.";
 RL Mol. Pharmacol. 55:1101-1107(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
 RX MEDLINE=20568725; PubMed=1118334;
 RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
 RT "Molecular cloning and characterization of a new human histamine
 RL receptor, HH4R.";
 RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).
 RC TISSUE=Thalamus;
 RX MEDLINE=21181559; PubMed=11284713;
 RA Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,
 RA Macia C., Ouvre C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.;
 RT "Genomic organization and characterization of splice variants of the
 RL human histamine H3 receptor.";
 RL Biochem. J. 355:279-288(2001).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
 RC VAL-280.
 RX MEDLINE=21953383; PubMed=11956964;
 RA Wiedemann P., Boenisch H., Oerters F., Brueess M.;
 RT "Structure of the human histamine H3 receptor gene (HRH3) and
 RL identification of naturally occurring variations.";
 RL J. Neural Transm. 109:443-453(2002).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Ullner C., Zirwes E., Lubbert H.;
 RT "Cloning and functional expression of the human histamine H3S
 RL receptor.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Aeburst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hamod S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharasath M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.J., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce R.D., Smith M.I., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
 CC histamine signals in CNS and peripheral nervous system. Signals
 CC through the inhibition of adenylylase cyclase and displays high
 CC constitutive activity (spontaneous activity in the absence of
 CC agonist). Agonist stimulation of isoform 3 neither modified
 CC adenylylase cyclase activity nor induced intracellular calcium
 CC mobilization.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:

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CC Event-Alternative splicing; Named isoforms=7;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q9Y5N1-1; Sequence=VSP_001886;
CC Name=2;
CC IsoId=Q9Y5N1-2; Sequence=VSP_001886;
CC Name=3; Synonym=H3S;
CC IsoId=Q9Y5N1-3; Sequence=VSP_001885;
CC Name=4;
CC IsoId=Q9Y5N1-4; Sequence=VSP_001881;
CC Name=5;
CC IsoId=Q9Y5N1-5; Sequence=VSP_001882;
CC Name=6;
CC IsoId=Q9Y5N1-6; Sequence=VSP_001883;
CC Name=7;
CC IsoId=Q9Y5N1-7; Sequence=VSP_001884;
CC -1- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the
CC greatest expression in the thalamus and caudate nucleus. The
CC various isoforms are mainly coexpressed in brain, but their
CC relative expression level varies in a region-specific manner.
CC Isoforms 3 and 7 are highly expressed in the thalamus, caudate
CC nucleus and cerebellum while isoforms 5 and 6 show a poor
CC expression. Isoforms 5 and 6 show a high expression in the
CC amygdala, substantia nigra, cerebral cortex and hypothalamus.
CC Isoform 7 is not found in hypothalamus or substantia nigra.
CC -1- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome
CC [MIM:146500]. This syndrome is characterized by orthostatic
CC hypotension, bladder and bowel incontinence, anhidrosis, iris
CC atrophy, amyotrophy, ataxia, rigidity and tremor.
CC -1- MISCELLANEOUS: Does not bind to cimetidine and triptolide. Shows
CC modest affinity for thioramidine, imetit, N-alpha-methylhistamine
CC and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to
CC iodoproxyfan while isoforms 1 and 3 bind it with high affinity.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 217 POTENTIAL.
FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 381 395 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 396 416 POTENTIAL.
FT DOMAIN 417 445 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 223 POLY-ALA.
FT DOMAIN 250 256 POLY-PRO.
FT DOMAIN 292 298 POLY-GLY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 85 98 Missing (in isoform 4).
FT VARSPLIC 197 315 Missing (in isoform 5).
FT VARSPLIC 227 342 Missing (in isoform 6).
FT VARSPLIC 234 263 Missing (in isoform 7).
FT VARSPLIC 274 353 Missing (in isoform 3).
FT VARSPLIC 445 445 K -> KKKKKTKCL (in isoform 2).
FT VARIANT 280 280 A -> V (IN SHY-DRAGER SYNDROME).
FT CONFLICT 19 19 E -> D (IN REF. 1 AND 5).
SQ SEQUENCE 445 AA; 48671 MM; 2ACF7440FBE95B6C CRC64;

Query Match 2.8%; Score 11; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LNLAISDFLWG 65
Db 74 LNLAISDFLWG 84

RESULT 4
ID_H3R_MOUSE STANDARD; PRT; 445 AA.
AC P59406;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
GN HRH3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RA Coqe F., Rigue H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,
RA Galizzi J.-P.;
RL "Cloning of mouse histamine H3 receptor.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBB databases.
CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC EMBL; AY044153; AAK72406.1; --
DR MGD; MGI:2139279; Hrb3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 61 70 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 109 129 POTENTIAL.
FT DOMAIN 130 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 217 POTENTIAL.
FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 381 396 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 397 417 POTENTIAL.
FT DOMAIN 418 445 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 20 23 POLY-ALA.
SQ SEQUENCE 445 AA; 48541 MW; 8BD406E29E1F3C5F CRC64;

Query Match 2.8%; Score 11; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLATSDFLVG 65
Db 74 LNLATSDFLVG 84

RESULT 5
HH3R_RAT
ID HH3R_RAT STANDARD; PRT; 445 AA.
AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN HH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hypothalamus;
RX MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species
pharmacological profiles.";
RL J. Pharmacol. Exp. Ther. 293:771-778 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Striatum;
RX MEDLINE=21016732; PubMed=11130725;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
RA Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
RT "High constitutive activity of native H3 receptors regulates histamine
neurons in brain.";
RL Nature 408:860-864 (2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RA Itadani H., Takimura T., Nakamura T., Ohta M.;
RT "Cloning of a novel G protein-coupled receptor.";

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RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
receptor.";
RL Mol. Pharmacol. 55:1101-1107 (1999).
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
histamine signals in CNS and peripheral nervous system. Signals
through the inhibition of adenylyl cyclase and displays high
constitutive activity (spontaneous activity in the absence of
agonists).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
Name=1; Synonyms=H3L;
IsoId=Q9QYN8-1; Sequence=Displayed;
Name=2; Synonyms=H3S;
IsoId=Q9QYN8-2; Sequence=VSP_001887;
Name=3;
IsoId=Q9QYN8-3; Sequence=VSP_001888;
Name=4;
IsoId=Q9QYN8-4; Sequence=VSP_001888, VSP_001889;
CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain, most notably
throughout the thalamus, the ventromedial hypothalamus and the
caudate nucleus. Isoform 1 is largely predominant in all tissues.
CC -!- MISCELLANEOUS: Proxifan acts as a potent neutral antagonist while
thiopramide, ciproxifan and FUB465 act as potent inverse
agonists.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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or send an email to license@isb-sib.ch).

EMBL; AF237919; AAF82086.1; -
DR EMBL; AY009370; AAK02069.1; -
DR EMBL; AB015646; BAA88765.1; -
DR EMBL; AB015646; BAA88766.1; -
DR EMBL; AB015646; BAA88767.1; -
DR EMBL; AB015646; BAA88768.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003980; H3_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Alternative splicing.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 60 POTENTIAL.
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 91 POTENTIAL.
FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 109 129 POTENTIAL.
FT DOMAIN 130 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 217 POTENTIAL.
FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 381 396 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 397 417 POTENTIAL.
FT DOMAIN 418 445 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 23 POLY-ALA.

```


FT	DOMAIN	190	220	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	221	241	5 (POTENTIAL).
FT	DOMAIN	242	270	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	271	291	6 (POTENTIAL).
FT	DOMAIN	292	310	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	311	331	7 (POTENTIAL).
FT	DOMAIN	332	381	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	7	7	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	24	24	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	125	205	BY SIMILARITY.
FT	CONFLICT	244	244	S -> P (IN REF. 3).
FT	CONFLICT	375	375	V -> L (IN REF. 2); BAC26971).
SQ	SEQUENCE	381 AA; 43375 MW;	1981FDL01324166D CRC64;	

Query Match 2.3%; Score 9; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	56	NLAISDFLV 64	
Db	91	NLAISDFLV 99	

RESULT 8

ID	PKR2 RAT	STANDARD;	PRT;	383 AA.
AC	Q8R415;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Prokineticin receptor 2 (PK-R2) (G protein-coupled receptor 73-like 1)			
DE	(G protein-coupled receptor 15E).			
GN	GRP73L1 OR PKR2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NCBI	TaxID=10116;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RX	MEDLINE=22050031; PubMed=12054613;			
RA	Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,			
RA	Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,			
RA	Inatomi N., Ohnaki T., Onda H., Fujino M.;			
RT	"Isolation and identification of EG-VEGF/prokineticins as cognate			
RL	ligands for two orphan G-protein-coupled receptors.";			
RL	Biochem. Biophys. Res. Commun. 293:396-402(2002).			
CC	-[1- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the			
CC	G(q) subclass of heteromeric G proteins. Activation leads to			
CC	mobilization of calcium, stimulation of phosphoinositide turnover			
CC	and activation of calcium, stimulation of phosphoinositide turnover			
CC	(similarity).			
CC	-[1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-[1- TISSUE SPECIFICITY: Abundantly expressed in the CNS and			
CC	reproductive organs with the highest levels in the cerebrum,			
CC	cerebellum, testis and ovary.			
CC	-[1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			

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EMBL: AY089975; AAM11891.1; ALT_INIT.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP FL 2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.

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DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1. Glycoprotein.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 54 74 1 (POTENTIAL).
FT DOMAIN 75 89 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 90 110 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 111 136 2 (POTENTIAL).
FT TRANSMEM 137 157 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 158 170 3 (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 222 5 (POTENTIAL).
FT TRANSMEM 223 243 6 (POTENTIAL).
FT DOMAIN 244 272 7 (POTENTIAL).
FT TRANSMEM 273 293 8 (POTENTIAL).
FT DOMAIN 294 312 9 (POTENTIAL).
FT TRANSMEM 313 333 10 (POTENTIAL).
FT DOMAIN 334 383 11 (POTENTIAL).
FT TRANSMEM 384 413 12 (POTENTIAL).
FT CARBOHYD 7 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 128 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 383 AA; 43603 MW; 477C501099535B93 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64
DB 94 NLAISDFLV 102

RESULT 9
PKR2_BOVIN
ID PKR2_BOVIN STANDARD; PRT; 384 AA.
AC Q8SPN1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (G protein-coupled receptor 15E).
DE (G protein-coupled receptor 15E).
GN GPR73L1 OR PKR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22050031; PubMed=12054613;
RA Masuda Y., Takatsu Y., Teruo Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors."
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the
CC G(q) subclass of heteromeric G proteins. Activation leads to
CC mobilization of calcium, stimulation of phosphoinositide turnover
CC and activation of p44/p42 mitogen-activated protein kinase (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY089973; AAM11889.1; .
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
DR

```

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker R., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A.C., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.B., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RL "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the
CC G(q) subclass of heteromeric G proteins. Activation leads to
CC mobilization of calcium, stimulation of phosphoinositide turnover
CC and activation of p44/p42 mitogen-activated protein kinase.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the ileocecum, thyroid gland,
CC pituitary gland, salivary gland, adrenal gland, testis, ovary and
CC brain.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF506288; AAM48128.1; -;
CC EMBL; AB084081; BAC24022.1; -;
CC EMBL; AL121755; CAB89854.1; ALT_SEQ.
CC DR Genew; HGNC:15836; GPR7311.
CC DR MIM; 607123;
CC DR InterPro; IPR000276; GPCR_Rhodpsn.
CC DR Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS; PR00237; GPCRHHODPSN.
CC DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 55 75 1 (POTENTIAL).
CC FT DOMAIN 76 89 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 90 110 2 (POTENTIAL).
CC FT DOMAIN 111 136 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 137 157 3 (POTENTIAL).
CC FT DOMAIN 158 171 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 172 192 4 (POTENTIAL).
CC FT DOMAIN 193 223 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 224 244 5 (POTENTIAL).
CC FT DOMAIN 245 273 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 274 294 6 (POTENTIAL).
CC FT DOMAIN 295 313 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 314 334 7 (POTENTIAL).
CC FT DOMAIN 335 384 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 7
CC FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 128 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 384 AA; 43995 MW; 2D5BFA3655347B5E CRC64;

Query Match 2.3%; Score 9; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 NLAISDFLV 64
DB 94 NLAISDFLV 102
|||||
RESULT 11
PARI BOVIN
ID PKR1 BOVIN STANDARD; PRT; 393 AA.
AC Q8SPN2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)
DE (G protein-coupled receptor ZAQ).
GN GPR73 OR PKR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22050031; PubMed=12054613;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohkaki T., Onda H., Fujino M.,
RT "Isolation and identification of EG-VGFP/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the
CC G(q) subclass of heteromeric G proteins. Activation leads to
CC mobilization of calcium, stimulation of phosphoinositide turnover
CC and activation of p44/p42 mitogen-activated protein kinase (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY089972; AAM11888.1; -;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS; PR00237; GPCRHHODPSN.
CC DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 63 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 64 84 1 (POTENTIAL).
CC FT DOMAIN 85 98 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 99 119 2 (POTENTIAL).
CC FT DOMAIN 120 145 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 146 166 3 (POTENTIAL).
CC FT DOMAIN 167 179 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 180 200 4 (POTENTIAL).
CC FT DOMAIN 201 232 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 233 253 5 (POTENTIAL).
CC FT DOMAIN 254 282 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 283 303 6 (POTENTIAL).
CC FT DOMAIN 304 322 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 323 343 7 (POTENTIAL).
CC FT DOMAIN 344 393 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 137 217 BY SIMILARITY.

Mon Oct 4 10:27:26 2004

SQ SEQUENCE 393 AA; 44602 MW; CF302DD364D8A2CC CRC64;
 Query Match 2.3%; Score 9; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 56 NLAISDFLV 64
 DB 103 NLAISDFLV 111
 RESULT 12
 PKR1 HUMAN STANDARD; PRT; 393 AA.
 ID PKR1 HUMAN STANDARD; PRT; 393 AA.
 AC Q8TCW9; Q8NRPJ7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)
 DE (GPR73a) (G protein-coupled receptor ZAQ).
 GN GPR73 OR PKR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22050031; PubMed=12054613;
 RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ighibashi Y., Suenaga M.,
 RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
 RA Inatomi N., Ohtaki T., Onda H., Fujino M.,
 RA "Isolation and identification of EG-VEGF/prokineticins as cognate
 RT ligands for two orphan G-protein-coupled receptors."
 RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22314729; PubMed=12427552;
 RA Soga T., Matsumoto S.-I., Oda T., Saito T., Hiyama H., Takasaki J.,
 RA Kamohara M., Ohishi T., Matsushine H., Furuichi K.;
 RA "Molecular cloning and characterization of prokineticin receptors."
 RL Biochim. Biophys. Acta 1579:173-179(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22028034; PubMed=11868676;
 RA Lin D.C.-H., Bullock C.M., Ehler F.J., Chen J.-L., Tian H.,
 RA Zhou Q.-Y.;
 RA "Identification and molecular characterization of two closely related
 RT G protein-coupled receptors activated by prokineticins/endocrine gland
 RT vascular endothelial growth factor."
 RL J. Biol. Chem. 277:19276-19280(2002).
 CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the
 CC G(q) subclass of heteromeric G proteins. Activation leads to
 CC mobilization of calcium, stimulation of phosphoinositide turnover
 CC and activation of p44/p42 mitogen-activated protein kinase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the stomach, throughout the small
 CC intestine, colon, rectum, thyroid gland, pituitary gland, salivary
 CC gland, adrenal gland, testis, ovary, brain, spleen, prostate and
 CC pancreas.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AY089976; AA011892.1; -
 CC EMBL; AB084080; BAC24021.1; -
 CC EMBL; AF506287; AA048127.1; -
 CC Genew; HGNC:4524; GPR73.

MIM; 607122; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 2; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR; Transmembrane; Glycoprotein.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 62
 FT TRANSMEM 63 83
 FT DOMAIN 84 98
 FT TRANSMEM 99 119
 FT DOMAIN 120 146
 FT TRANSMEM 147 167
 FT DOMAIN 168 180
 FT TRANSMEM 181 201
 FT DOMAIN 202 232
 FT TRANSMEM 233 253
 FT DOMAIN 254 282
 FT TRANSMEM 283 303
 FT DOMAIN 304 322
 FT TRANSMEM 323 343
 FT DOMAIN 344 393
 FT CARBOHYD 11 11
 FT CARBOHYD 14 14
 FT CARBOHYD 36 36
 FT DISULFID 137 217
 FT CONFLICT 255 256
 SQ SEQUENCE 393 AA; 44769 MW; 0D36461CA99CAEC1 CRC64;
 Query Match 2.3%; Score 9; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 56 NLAISDFLV 64
 DB 103 NLAISDFLV 111
 RESULT 13
 PKR1 MOUSE STANDARD; PRT; 393 AA.
 ID PKR1 MOUSE STANDARD; PRT; 393 AA.
 AC Q9UKL1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73).
 GN GPR73 OR PKR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20225484; PubMed=10760605;
 RA Parker R., Liu M., Eyre H.J., Copeland N.G., Gilbert D.J.,
 RA Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
 RA "v-receptor-like genes GPR72 and GPR73: molecular cloning, genomic
 RT organisation and assignment to human chromosome 11q21.1 and p14 and
 RT mouse chromosome 9 and 6."
 RL Biochim. Biophys. Acta 1491:369-375(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE=22022134; PubMed=12024206;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
 RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
 RA "Prokineticin 2 transmits the behavioural circadian rhythm of the
 RT suprachiasmatic nucleus."
 RL Nature 417:405-410(2002).
 CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the
 CC G(q) subclass of heteromeric G proteins. Activation leads to
 CC mobilization of calcium, stimulation of phosphoinositide turnover

CC and activation of p44/p42 mitogen-activated protein kinase (By
CC similarity).
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- TISSUE SPECIFICITY: Expressed at high levels in the heart, skeletal
CC muscle and pancreas. Expressed at lower levels in the brain, lung,
CC liver and kidney.
CC
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF236082; AAF43706.1; -
CC EMBL; AF487278; AAM49570.1; -
CC MGD; MGI:1929676; Gpr73.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 63 83 1 (POTENTIAL).
CC FT DOMAIN 84 98 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 99 119 2 (POTENTIAL).
CC FT DOMAIN 120 146 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 147 167 3 (POTENTIAL).
CC FT DOMAIN 168 179 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 180 200 4 (POTENTIAL).
CC FT DOMAIN 201 232 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 233 253 5 (POTENTIAL).
CC FT DOMAIN 254 282 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 283 303 6 (POTENTIAL).
CC FT DOMAIN 304 322 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 323 343 7 (POTENTIAL).
CC FT DOMAIN 344 393 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 137 217 BY SIMILARITY.
CC SEQUENCE 393 AA; 44528 MW; 46F5E78C00DC871C CRC64;

Query Match 2.3%; Score 9; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64
DB 103 NLAISDFLV 111
ID PKR1 RAT STANDARD; PRT; 393 AA.
AC Q8P4L6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)
DE (G protein-coupled receptor ZAQ).
GN GPR73 OR PKR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,

RESULT 14

PKR1 RAT

ID PKR1 RAT

AC Q8P4L6;

DT 10-OCT-2003

DT 10-OCT-2003

DE Prokineticin receptor 1

DE (G protein-coupled receptor 73)

GN GPR73 OR PKR1.

OS Rattus norvegicus

OC Eukaryota;

OC Mammalia;

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=22050031;

RA Masuda Y., Takatsu Y.,

RA Abe M., Fukusumi S.,

RA Watanabe T., Shintani Y.,

RA Yamada T., Hinuma S.,

RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RL ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the
CC G(q) subclass of heteromeric G proteins. Activation leads to
CC mobilization of calcium, stimulation of phosphoinositide turnover
CC and activation of p44/p42 mitogen-activated protein kinase (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in peripheral tissues with
CC the highest level in the spleen and moderate levels in the adipose
CC tissues, thymus, lung, kidney, testis, uterus and small intestine.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY089974; AAM11890.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 63 83 1 (POTENTIAL).
CC FT DOMAIN 84 98 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 99 119 2 (POTENTIAL).
CC FT DOMAIN 120 145 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 146 166 3 (POTENTIAL).
CC FT DOMAIN 167 179 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 180 200 4 (POTENTIAL).
CC FT DOMAIN 201 232 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 233 253 5 (POTENTIAL).
CC FT DOMAIN 254 282 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 283 303 6 (POTENTIAL).
CC FT DOMAIN 304 322 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 323 343 7 (POTENTIAL).
CC FT DOMAIN 344 393 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 137 217 BY SIMILARITY.
CC SEQUENCE 393 AA; 44507 MW; C75EC72B97E503A8 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64

DB 103 NLAISDFLV 111

ID OPD CAMAB STANDARD; PRT; 378 AA.

AC Q17292;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE Rhodopsin.

DE Rhodopsin.

OS Camponotus abdominalis (Carpenter ant).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;

OC Formicidae; Formicidae; Camponotus.

OX NCBI_TaxID=47731;

RN [1]

RP SEQUENCE FROM N.A.

Mon Oct 4 10:27:26 2004

us-10-626-445-8.olog.rsp

```

RC TISSUE=Retina;
RX MEDLINE=98039419; PubMed=9372150;
RA Popp M.P., Grishammer R., Hargrave P.A., Smith W.C.;
RT "Ant. opsins: sequences from the Saharan silver ant and the carpenter
ant.";
RL Invertebr. Neurosci. 1:323-329(1996).
CC -!- FUNCTION: Visual pigments are the light-absorbing molecules that
CC mediate vision. They consist of an apoprotein, opsin, covalently
CC linked to cis-retinal.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Some or all of the carboxyl-terminal Ser or Thr residues may
CC be phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Opsin subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; U32502; AAC47083.1; -.
DR HSP; P02699; IF88.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001760; Opsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00238; OPSIN; 1.
DR Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; G-protein coupled receptor.
FT DOMAIN 1 53
FT TRANSMEM 54 78
FT DOMAIN 79 90
FT TRANSMEM 91 115
FT DOMAIN 116 130
FT TRANSMEM 131 150
FT DOMAIN 151 169
FT TRANSMEM 170 193
FT DOMAIN 194 217
FT TRANSMEM 218 245
FT DOMAIN 246 280
FT TRANSMEM 281 304
FT DOMAIN 305 311
FT TRANSMEM 312 336
FT DOMAIN 337 378
FT TRANSMEM 379 404
FT BINDING 323 323
FT CARBOHYD 24 24
FT CARBOHYD 200 200
FT SEQUENCE 378 AA; 42091 MW; 99C95CB5093BA433 CRC64;
Query Match 2.0%; Score 8; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 NLAISDFL 63
DB 95 NLAISDFL 102

```

Search completed: October 1, 2004, 10:26:53
 Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:20:40 ; Search time 118 Seconds
(without alignments)
1045.488 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKPALSQNSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	379	96.9	391	11	Q91ZY2	Q91zy2 mus musculus
2	33	8.4	391	11	Q91ZY1	Q91zy1 rattus norv
3	32	8.2	389	11	Q91ZY3	Q91zy3 cavia porce
4	21	5.4	390	4	Q96LD9	Q96ld9 homo sapien
5	16	4.1	390	6	Q8WNV9	Q8wnv9 sus scrofa
6	11	2.8	147	6	Q865E3	Q865e3 canis fami
7	11	2.8	200	4	Q8NI50	Q8ni50 homo sapien
8	11	2.8	301	4	Q8WY00	Q8wy00 homo sapien
9	11	2.8	309	4	Q8NI49	Q8ni49 homo sapien
10	11	2.8	365	4	Q8WY01	Q8wy01 homo sapien
11	11	2.8	373	4	Q8WY29	Q8wx29 homo sapien
12	11	2.8	445	6	Q865E1	Q865e1 macaca mla
13	8	2.0	79	10	Q84PJ1	Q84pj1 goessypioide
14	8	2.0	150	2	Q9FL30	Q9fl30 pseudomonas
15	8	2.0	181	4	Q9BQJ4	Q9bqj4 homo sapien
16	8	2.0	181	6	Q9XSV3	Q9xsv3 canis fami

17	8	2.0	181	11	Q9JJG6	Q9jjg6 mus musculu
18	8	2.0	278	3	Q871W9	Q871w9 neurospora
19	8	2.0	281	16	Q8YDR4	Q8ydr4 bruceella me
20	8	2.0	281	16	Q8FUN6	Q8fun6 bruceella su
21	8	2.0	292	16	Q98JZ0	Q98jz0 rhizobium l
22	8	2.0	314	16	Q8EJK3	Q8ejk3 streptococc
23	8	2.0	314	16	Q8DXY4	Q8dxy4 streptococc
24	8	2.0	328	5	Q20759	Q20759 caenorhabdi
25	8	2.0	368	10	Q43153	Q43153 spinacia ol
26	8	2.0	396	16	Q7WD90	Q7wd90 bordetella
27	8	2.0	396	16	Q7W5Q4	Q7w5q4 bordetella
28	8	2.0	396	16	Q7VW94	Q7vw94 bordetella
29	8	2.0	400	2	O52293	Q52293 pseudomonas
30	8	2.0	400	16	Q88E05	Q88e05 pseudomonas
31	8	2.0	426	16	Q9RYQ3	Q9ryq3 deinococcus
32	8	2.0	457	16	Q7WJ42	Q7wj42 bordetella
33	8	2.0	527	10	Q94HB1	Q94hb1 oryza sativ
34	8	2.0	534	13	O57422	O57422 xenopus lae
35	8	2.0	672	10	Q94D59	Q94d59 oryza sativ
36	8	2.0	902	5	Q86198	Q86198 dictyosteli
37	8	2.0	1188	16	Q8E9K4	Q8e9k4 shewanella
38	8	2.0	9271	5	Q8IES7	Q8ies7 plasmodium
39	7	1.8	55	16	Q8YNG1	Q8yng1 anabaena sp
40	7	1.8	72	6	Q866B5	Q866b5 cebus apell
41	7	1.8	80	4	Q8TDP5	Q8tdp5 homo sapien
42	7	1.8	82	4	Q8TDP6	Q8tdp6 homo sapien
43	7	1.8	93	10	Q8H1V0	Q8h1v0 mirabilis j
44	7	1.8	98	16	Q8YXH9	Q8yxh9 anabaena sp
45	7	1.8	100	17	Q8PZT9	Q8pzt9 methanosarc

ALIGNMENTS

RESULT 1

Q91ZY2 ID Q91ZY2 PRELIMINARY; PRT; 391 AA.
AC Q91ZY2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H4 receptor.
GN HRH4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
suggests substantial species variation."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF358859; AAK97380.1; -;
DR MGD; MGI:2429635; Hrha4.
DR GO; GO:0005887; C:integral to plasma membrane; IC.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0004969; F:histamine receptor activity; IDA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008102; Histamine_H4.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00462; G-PROTEIN RECEPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;
Query Match 96.9%; Score 379; DB 11; Length 391;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFIMSSFAIMVGNVAVWILAFVVDRLHRNSYFFLNLAIS 60
 DB 1 MSESNTGILPPAAQVPLAFIMSSFAIMVGNVAVWILAFVVDRLHRNSYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLLCTASVYNNVLISDYRYQSVNAV 120
 DB 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLLCTASVYNNVLISDYRYQSVNAV 120

QY 121 SYRAQHTGIMKIVAQWAVWILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180
 DB 121 SYRAQHTGIMKIVAQWAVWILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180

QY 181 MLLEFLPLFVSVAYFNVQIYWSLWKRRALSRCPHAGSFSTSSASGHLHRAGVACRTSN 240
 DB 181 MLLEFLPLFVSVAYFNVQIYWSLWKRRALSRCPHAGSFSTSSASGHLHRAGVACRTSN 240

QY 241 PGLKESAAHRSSEPRKSSILVSLRTHMNSSITAFKVGSPWRSBAALROREYAEALLRG 300
 DB 241 PGLKESAAHRSSEPRKSSILVSLRTHMNSSITAFKVGSPWRSBAALROREYAEALLRG 300

QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPLY 360
 DB 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPLY 360

QY 361 PLCHRRFQKAPWKILCVTK 379
 DB 361 PLCHRRFQKAPWKILCVTK 379

RESULT 2
 Q91ZY1 PRELIMINARY; PRT; 391 AA.
 AC Q91ZY1; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histamine H4 receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
 RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
 RT suggests substantial species variation."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF358860; AAK97381.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 391 AA; 44023 MW; C707BAE39CFED41 CRC64;

Query Match 8.4%; Score 33; DB 11; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.3e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 KIVAQMVAWVILAFVNGPMLASDSWKNSTNT 163
 DB 131 KIVAQMVAWVILAFVNGPMLASDSWKNSTNT 163

Db 131 KIVAQMVAWVILAFVNGPMLASDSWKNSTNT 163

RESULT 3
 Q91ZY3 PRELIMINARY; PRT; 389 AA.
 AC Q91ZY3; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histamine H4 receptor.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
 RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
 RT suggests substantial species variation."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF358858; AAK97379.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008102; Histamine_H4.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSIN.
 DR PROSITE; PR01726; HISTAMINEH4.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 389 AA; 44511 MW; 51AF32FD6F1C3E4F CRC64;

Query Match 8.2%; Score 32; DB 11; Length 389;
 Best Local Similarity 100.0%; Pred. No. 1.4e-24;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 FMLITDYLLCTASVYNNVLISDYRYQSVNAV 120
 DB 88 FMLITDYLLCTASVYNNVLISDYRYQSVNAV 119

RESULT 4
 Q96LD9 PRELIMINARY; PRT; 390 AA.
 AC Q96LD9; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histamine receptor H4.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nguyen T., George S.R., Lee D.K., Cheng R., Lynch K.R., O'Dowd B.F.;
 RT "Discovery of H4, a Novel Histamine Receptor."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AY008280; AAL09297.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.

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DR InterPro: IPR008102; Histamine_H4.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR01726; HISTAMINEH4R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44469 MW; CC82BD5D30D216C66 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 390;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVNVILISDRY 113
Db 93 TDYLLCTASVNVILISDRY 113
|||||

RESULT 5
ID Q8WNV9 PRELIMINARY; PRT; 390 AA.
AC Q8WNV9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.;
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DE EMBL: A8053300; BAB83078.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR01726; HISTAMINEH4R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;

Query Match
Best Local Similarity 100.0%; Score 16; DB 6; Length 390;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 DYLLCTASVNVILIS 109
Db 96 DYLLCTASVNVILIS 111
|||||

RESULT 6
ID Q865E3 PRELIMINARY; PRT; 147 AA.
AC Q865E3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine receptor H3 (fragment).
GN HRH3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Witte D.G., Esbenshade T.A., Hancock A.A., Yao B.B.;
RT "The canine histamine receptor H3 (HRH3) partial cDNA sequence.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY231115; AA083755.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003980; H3_receptor.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW Receptor.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 16900 MW; 67F6A741B518854E CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 147;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LNLAISDFLVG 65
Db 3 LNLAISDFLVG 13
|||||

RESULT 7
ID Q8NI50 PRELIMINARY; PRT; 200 AA.
AC Q8NI50;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 5.
GN HRH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
DR EMBL: AF346903; AAM43828.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003980; H3_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
SQ SEQUENCE 200 AA; 21612 MW; 2038D14BC186D1EA CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 200;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR	EMBL; AF346904; AAM43829.1; "
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0004969; F:histamine receptor activity; IEA.
DR	GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR	InterPro; IPR00276; GPCR_Rhodpsn.
DR	InterPro; IPR003980; H3_receptor.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODOPSN.
DR	PRINTS; PR01471; HISTAMINEH3R.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor.
SQ	SEQUENCE 309 AA; 34242 MW; B7496F7D1D2A206B CRC64;
Query Match	2.8%; Score 11; DB 4; Length 309;
Best Local Similarity	100.0%; Pred.No. 0.014;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	55 LNLAISDFLVG 65
Db	74 LNLAISDFLVG 84
RESULT 10	
ID	Q8WY01 PRELIMINARY; PRT; 365 AA.
AC	Q8WY01
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Histamine H3 receptor isoform 2.
GN	HRH3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Hippocampus;
RA	Weinendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA	Weiner D.M.;
RT	"Molecular Cloning and Characterization of Functionally Distinct
RT	Isoforms of the Human Histamine H3 Receptor.";
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF321911; AAL71912.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0004969; F:histamine receptor activity; IEA.
DR	GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR	InterPro; IPR00276; GPCR_Rhodpsn.
DR	InterPro; IPR003980; H3_receptor.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODOPSN.
DR	PRINTS; PR01471; HISTAMINEH3R.
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Histamine H3 receptor isoform 6.
GN	HRH3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Hippocampus;
RA	Weinendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA	Weiner D.M.;
RT	"Molecular Cloning and Characterization of Functionally Distinct
RT	Isoforms of the Human Histamine H3 Receptor.";
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF321912; AAL71913.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0004969; F:histamine receptor activity; IEA.
DR	GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR	InterPro; IPR00276; GPCR_Rhodpsn.
DR	InterPro; IPR003980; H3_receptor.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODOPSN.
DR	PRINTS; PR01471; HISTAMINEH3R.
DT	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DT	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor.
SQ	SEQUENCE 301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;
Query Match	2.8%; Score 11; DB 4; Length 301;
Best Local Similarity	100.0%; Pred.No. 0.014;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	55 LNLAISDFLVG 65
Db	74 LNLAISDFLVG 84
RESULT 9	
ID	Q8NI49 PRELIMINARY; PRT; 309 AA.
AC	Q8NI49
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Histamine H3 receptor isoform 6.
GN	HRH3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Hippocampus;
RA	Weinendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA	Weiner D.M.;
RT	"Molecular Cloning and Characterization of Functionally Distinct
RT	Isoforms of the Human Histamine H3 Receptor.";
RL	Neuropharmacology 0:0-0(2002).

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SQ SEQUENCE 150 AA; 17439 MW; 8AAC59D07FD6E83B CRC64;

Query Match 2.0%; Score 8; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 CRTSNPGL 243
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Db 7 CRTSNPGL 14

RESULT 15

Q9BQJ4 PRELIMINARY; PRT; 181 AA.

AC Q9BQJ4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Brain cell membrane protein 1).
GN DKFZP761J17121.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amygdala;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiesmann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoerge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
EL Genome Res. 11:422-435 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL136550; CAB66485.1; -;
DR EMBL; BC039242; AAH39242.1; -;
SQ SEQUENCE 181 AA; 19997 MW; A73A03FD0C3B3FBB CRC64;

Query Match 2.0%; Score 8; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 FLVGLISI 69
| | | | | | | |
Db 96 FLVGLISI 103

Search completed: October 1, 2004, 10:28:58
Job time : 120 secs